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FILE COVERS 1967 - 8 May 1996 (960508/ED) VOL 124 ISS 20

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Thesauri are now available for the WIPO International Patent Classifications (IPC) editions 1-6 in the /IC1, /IC2, /IC3, /IC4, /IC5, and /IC (/IC6) fields, respectively. The thesauri in the /IC5 and /IC fields also include the corresponding catchword terms from the IPC subject headings and subheadings.

- L1 40 SEA FILE=REGISTRY GAAGTTCCTATTC/SQSN
 L2 34 SEA FILE=REGISTRY GTATAGGAACTTC/SQSN
 L3 29 SEA FILE=REGISTRY L1(L)L2
 L4 5 SEA FILE=HCA L3
- L4 ANSWER 1 OF 5 HCA COPYRIGHT 1996 ACS
- AN 123:331869 HCA
- TI The role of DNA bending in Flp-mediated site-specific recombination
- AU Luetke, Karen H.; Sadowski, Paul D.
- CS Dep. Molecular and Medical Genetics, Univ. Toronto, Toronto, ON, M5S 1A8, Can.
- SO J. Mol. Biol. (1995), 251(4), 493-506 CODEN: JMOBAK; ISSN: 0022-2836
- DT Journal
- LA English
- L4 ANSWER 2 OF 5 HCA COPYRIGHT 1996 ACS
- AN 121:126321 HCA
- TI In vivo excision and amplification of large segments of the Escherichia coli genome
- AU Posfai, Gyorgy; Koob, Michael; Hradecna, Zdenka; Hasan, Noaman; Filutowicz, Marcin; Szybalski, Waclaw
- CS McArdle Lab. Cancer Res., Univ. Wisconsin, Madison, WI, 53706, USA
- SO Nucleic Acids Res. (1994), 22(12), 2392-8 CODEN: NARHAD; ISSN: 0305-1048
- DT Journal
- LA English
- L4 ANSWER 3 OF 5 HCA COPYRIGHT 1996 ACS
- AN 119:198292 HCA
- TI Ligation of synthetic activated DNA substrates by site-specific recombinases and topoisomerase I

- Að 'Guohua; Luetke, Karen; Juby, Carl D.; Brousseau, Roland; Sadowski, Paul
- CS Dep. Mol. Med. Genet., Univ. Toronto, Toronto, ON, M5S 1A8, Can.
- SO J. Biol. Chem. (1993), 268(5), 3683-9 CODEN: JBCHA3; ISSN: 0021-9258
- DT Journal
- LA English
- L4 ANSWER 4 OF 5 HCA COPYRIGHT 1996 ACS
- AN 114:1432 HCA
- TI Nucleotide sequence of a gene which enhances the activity of glyoxalase I in Saccharomyces cerevisiae
- AU Inoue, Yoshiharu; Feng, Ling; Bong-Young, Choi; Ginya, Harumi; Murata, Kousaka; Kimura, Akira
- CS Res. Inst. Food Sci., Kyoto Univ., Uji, 611, Japan
- SO Biotechnol. Appl. Biochem. (1990), 12(3), 341-5 CODEN: BABIEC; ISSN: 0885-4513
- DT Journal
- LA English
- L4 ANSWER 5 OF 5 HCA COPYRIGHT 1996 ACS
- AN 94:12618 HCA
- TI Nucleotide sequence of the yeast plasmid
- AU Hartley, James L.; Donelson, John E.
- CS Dep. Biochem., Univ. Iowa, Iowa City, IA, 52242, USA
- SO Nature (London) (1980), 286(5776), 860-5 CODEN: NATUAS; ISSN: 0028-0836
- DT Journal
- LA English

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

 n.a. database search, using Smith-Waterman algorithm n.a. Perch nn

Tue May 14 11:40:28 1996; MasPar time 2.46 Seconds 254.769 Million cell updates/sec Run on:

Tabular output not generated.

(1-34) from frt.seq 26 Perfect Score: Description:

1 qaaqttcctattcNNNNNNNNqtataggaacttc 34 N.A. Sequence: Comp:

cttcaaggataagNNNNNNNNcatatccttgaag

default TABLE Scoring table:

Gap 10

Dbase 0; Query 0 STD Nmatch

30947 seqs, 9219370 bases x 2 Searched:

Listing first 45 summaries Minimum Match 0% Post-processing:

Database:

n-issued 1:51 2:52 3:53 4:54 5:55 6:PCT90 7:PCT91 8:PCT92 9:PCT93 10:PCT94 11:PCT95 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Mean 5.064; Variance 2.619; scale 1.934

Statistics:

SUMMARIES

Pred. No. Applicatio Applicatio Applicatio Description Sequence 3, Sequence 4, Sequence 4, 8 Length Query Match 100.0 100.0 100.0 Score Result š.

2.38e-05 2.38e-05 2.38e-05 2.71e+00 2.71e+00 1.01e+01 1.01e+01 1.35e-08 1.35e-08 4.35e-08 Applicatio Applicatio Applicatio Applicatio Applicatio Applicatio Sequence 41, Applicati Sequence 3, Sequence 4, Sequence Sequence Sequence Sequence PCT-US92-0 PCT-US92-0 US-07-854-PCT-US92-0 PCT-US92-0 PCT-US93-0 US-08-292-US-07-991-US-07-854-PCT-US93-0 7859 1947 1997 1065 1689 84.6 84.6 84.6 53.8 50.0 50.0 26 26 27 27 27 27 27 27 27 27 31 31 31

PatentIn Release #1.0, Version #1.25

COMPUTER READABLE FORM:
HEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palace

USA

COUNTRY:

H.P.m. May 14 11.31

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Sequence 2, Applicatio Sequence 2, Applicatio	2,	24,	15,	4,	s,	 ì	'n,	5,	1, 4	18,	4,	Sequence 1, Applicatio	m,	4,	ο,	ຕັ	Sequence 54, Applicati	Sequence 3, Applicatio	2,	'n	ټ.	222		79, A	111,	111,	S,	Sequence 1, Applicatio	38,	38,	15,	'n	Sequence 1, Applicatio
US-07-998- Seq US-08-463- Seq	PCT-US92-1 Seq				PCT-US95-0 Seq	PCT-US93-0 Seq	PCT-US94-1 Seq	PCT-US94-1 Seq			US-07-753- Seq			US-08-278- Seq							PCT-US95-0 Seq					PCT-US95-0 Seq		US-08-278- Seq	PCT-US92-0 Seq	JS-07-872- Seq			PCT-US93-0 Seq
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ALI GNMENTS

MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL Sequence 3, Application PC/TUS9201899.
Sequence 3, Application PC/TUS9201899
GENERAL INFORMATION:
APPLICANT: WAHL, DR., GEOFFREY M.
APPLICANT: O'GORMAN DR., STEPHEN V.
TITLE OF INVENTION: FLP-MEDIATE GENE MODIFICATION IN
TITLE OF INVENTION: MAMMALIAN CELLS, AND COMPOSITIONS
TITLE OF INVENTION: THEREFOR ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK STREET: 444 South Flower Street, Suite 2000 CITY: Los Angeles H. PCT-US92-01899-3 STANDARD; DNA; UNC; 34 CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: ర STATE: 01-JAN-1900 XXXXXX RESULT

APPLICANT: WAHL, DR., GEOFFREY M.
APPLICANT: O'CORMAN DR., STEPHEN V.
ITILE OF INVENTION: FIP-MEDIATED GENE MODIFICATION IN
TITLE OF INVENTION: MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL
TITLE OF INVENTION: THEREFOR ö Gaps ; 8; Indels 100.0%; Score 26; DB 8; Length 34; 76.5%; Pred. No. 4.35e-08; NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
STREET: 444 South Flower Street, Suite 2000 INDIVIDUAL ISOLATE: FLP recombination target site COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/01899
FILING DATE: 19920306 Sequence 34 BP; 11 A; 6 C; 6 G; 11 T; 0 other; 0; Mismatches 1 gaagttcctattcNNNNNNNNgtataggaacttc 34 1 GAAGTTCCTATTCTCTAGAAAGTATAGGAACTTC 34 PCT-US92-01899-4 STANDARD; DNA; UNC; 68 BP REFERENCE/DOCKET NUMBER: P31 8929
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: unknown APPLICATION NUMBER: PCT/US92/01899 CLASSIFICATION: 800 TYTORNEY/AGENT INFORMATION: NAME: REITER MR., STEPHEN E. REGISTRATION NUMBER: 31192 REFERENCE/DOCKET NUMBER: P31 8929 Sequence 4, Application PC/TUS9201899. Sequence 4, Application PC/TUS9201899 GENERAL INFORMATION: NAME: REITER MR., STEPHEN E. REGISTRATION NUMBER: 31192 ATTORNEY/AGENT INFORMATION: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk CURRENT APPLICATION DATA: FILING DATE: 19920306 Best Local Similarity 76.5%; 26; Conservative TOPOLOGY: unknown CDNA CITY: Los Angeles STATE: CA CLASSIFICATION: ORIGINAL SOURCE: COUNTRY: USA MOLECULE TYPE: ZIP: 90071 01-JAN-1900 Query Match XXXXXX Matches 88888888888888888888888888 쇰 ð

May 14 11:31

CC TELECOMMUNICATION INFORMATION:

Gaps .; 0 8; Indels Score 26; DB 8; Length 68; Pred. No. 4.35e-08; SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: ORIGINAL SOURCE: INDIVIDUAL ISOLATE: Synthetic oligonucleotide Sequence 68 BP; 19 A; 16 C; 14 G; 19 T; 0 other; TITLE OF INVENTION: Proteins and nucleic acids STREET: Ten South Wacker Drive, Suite 3000 0; Mismatches US-07-854-596B-4 STANDARD; DNA; UNC; 7859 BP 34 GAAGTTCCTATTCTCTAGAAGTATAGGAACTTC 67 1 gaagttcctattcNNNNNNNNgtataggaacttc 34 APPLICATION NUMBER: US/07/854,596B ADDRESSEE: Dr. John J. McDonnell COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS Sequence 4, Application US/07854596B. Sequence 4, Application US/07854596B Patent No. 5434073 GENERAL INFORMATION: APPLICANT: Czaplewski, Lloyd G REGISTRATION NUMBER: 26,949 REFERENCE/DOCKET NUMBER: 9; TELECOMMUNICATION INFORMATION: TELEPHONE: 312-715-1000 TELEFAX: 312-715-1234 APPLICANT: Dawson, Keith M APPLICANT: Hunter, Michael G TELEFAX: (619) 535-8949 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: TELEX: 910-221-5317 INFORMATION FOR SEQ ID NO: 4: TELEPHONE: (619) 535-9001 FILING DATE: 03-JUN-1992 ATTORNEY/AGENT INFORMATION: NAME: McDonnell, John J LENGTH: 7859 base pairs LENGTH: 68 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: unknown Query Match 100.0%; Best Local Similarity 76.5%; Matches 26; Conservative NUMBER OF SEQUENCES: 73 SEQUENCE CHARACTERISTICS CORRESPONDENCE ADDRESS: CLASSIFICATION: 435 nucleic acid TOPOLOGY: unknown MOLECULE TYPE: CDNA Chicago COUNTRY: USA ZIP: 60606 STATE: IL 01-JAN-1900 XXXXXX RESULT ID US 셤 888888888888888 ð

윤 გ g g APPLICANT: WAIL, DR., GEOFFREY M.
APPLICANT: O'GORMAN DR., STEPHEN V.
TITLE OF INVENTION: FLP-MEDIATED GENE MODIFICATION IN
TITLE OF INVENTION: MAMMALINN CELLS, AND COMPOSITIONS AND CELLS USEFUL
TITLE OF INVENTION: THEREFOR
NUMBER OF SUGUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
STREET: 444 South Flower Street, Suite 2000 ö Gaps .; 0 OTHER INFORMATION: /note= "sequence of plasmid pSW6" Sequence 7859 BP; 2317 A; 1656 C; 1600 G; 2286 T; 0 other; Query Match 100.0%; Score 26; DB 4; Length 7859; Best Local Similarity 76.5%; Pred. No. 4.35e-08; Aatches 26; Conservative 0; Mismatches 8; Indels INDIVIDUAL ISOLATE: FLP recombination target site Sequence 34 BP; 11 A; 6 C; 6 G; 11 T; 0 other; COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/01899
FILING DATE: 19920306
CLASSIFICATION: 800 3131 GAAGTICCTATICTCTAGAAGTATAGGAACTIC 3164 JT 4 PCT-US92-01899-3 STANDARD; DNA; UNC; 34 BP. REFERENCE/DOCKET NUMBER: P31 8929 TELECOMMUNICATION: Sequence 3, Application PC/TUS9201899. Sequence 3, Application PC/TUS9201899 ATTORNEY/AGENT INFORMATION: NAME: REITER MR., STEPHEN E. REGISTRATION NUMBER: 31192 NFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: TELEPHONE: (619) 535-9001 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk (619) 535-8949 NAME/KEY: misc feature LOCATION: 1..7859 LENGTH: 34 base pairs STRANDEDNESS: unknown STRANDEDNESS: single 26; Conservative TOPOLOGY: circular TYPE: NUCLEIC ACID MOLECULE TYPE: CDNA ORIGINAL SOURCE: TOPOLOGY: unknown MOLECULE TYPE: CDNA CITY: Los Angeles GENERAL INFORMATION: COUNTRY: USA ZIP: 90071 STATE: CA TELEFAX: 01-JAN-1900 Query Match XXXXXX RESULT 888888888 ð

May 14 11:31 HD/mi

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APPLICANT: WAHL, DR., GEOFFREY M.
APPLICANT: O'GORMAN DR., STEPHEN V.
TITLE OF INVENTION: FIR-MEDIATED GENE MODIFICATION IN
TITLE OF INVENTION: MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL.
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: ö ö Gaps Gaps ö ; 0 0; Mismatches 10; Indels 84.6%; Score 22; DB 8; Length 68; 70.6%; Pred. No. 2.38e-05; 0; Mismatches 10; Indels Score 22; DB 8; Length 34; Pred. No. 2.38e-05; ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK STREET: 444 South Flower Street, Suite 2000 SOFTWARE: PatentIn Release #1.0, Version #1.25 INDIVIDUAL ISOLATE: Synthetic oligonucleotide Sequence 68 BP; 19 A; 16 C; 14 G; 19 T; 0 other; 1 GAAGTTCCTATTCTCTAGAAAGTATAGGAACTTC 34 34 gaagttcctatacNNNNNNNNNgaataggaacttc 1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/01899
FILING DATE: 19920306 LT 5 PCT-US92-01899-4 STANDARD; DNA; 68 = = = = = REFERENCE/DOCKET NUMBER: P31 8929 Sequence 4, Application PC/TUS9201899. Sequence 4, Application PC/TUS9201899 GENERAL INFORMATION: OPERATING SYSTEM: PC-DOS/MS-DOS CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION: NAME: REITER MR., STEPHEN E. REGISTRATION NUMBER: 31192 COMPUTER: IBM PC compatible TELECOMMUNICATION INFORMATION INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: TELEPHONE: (619) 535-9001 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk TELEFAX: (619) 535-8949 STRANDEDNESS: unknown Query Match
Best Local Similarity 70.6%; Query Match 84.6%; Best Local Similarity 70.6%; LENGIH: 68 base pairs 24; Conservative TYPE: NUCLEIC ACID CDNA Los Angeles TOPOLOGY: unknown ORIGINAL SOURCE: USA MOLECULE TYPE: ZIP: 90071 STATE: CA COUNTRY: 01-JAN-1900 XXXXXX Matches

34 GAAGTTCCTATTCTCTAGAAAGTATAGGAACTTC 67

34 gaagttcctatacNNNNNNNNnaataggaacttc 1

XXXXXX

RESULT ID PCT AC xxx

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Matches

PCT-US93-01720-6 STANDARD; DNA; UNC; 1997 BP. Sequence 6, Application PC/TUS9301720.
Sequence 6, Application PC/TUS9301720
GENERAL INFORMATION:
APPLICANT: Renauld, Jean-Christophe
APPLICANT: Druez, Catherine NAME: Hanson, Norman D. REGISTRATION NUMBER: 30,946 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 688-9200 CORRESPONDENCE ADDRESS:
ADDRESSE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York TELEFAX: (212) 838-3884 INFORMATION FOR SEQ ID NO: 4: OPERATING SYSTEM: PC-DOS LENGTH: 1947 base pairs CURRENT APPLICATION DATA: SEQUENCE CHARACTERISTICS: Query Match 53.8%; Best Local Similarity 60.7%; SOFTWARE: Wordperfect STRANDEDNESS: single 17; Conservative COMPUTER: IBM PS/2 NUMBER OF SEQUENCES: TYPE: NUCLEIC ACID COUNTRY: USA FILING DATE: ZIP: 10022 01-JAN-1900 XXXXXX Matches RESULT
1D PC
AC xx
DT 01
DE Se
CC Se
CC C For g გ. ö Gaps ö OTHER INFORMATION: /note= "sequence of plasmid pSW6" Sequence 7859 BP; 2317 A; 1656 C; 1600 G; 2286 T; 0 other; Query Match 84.6%; Score 22; DB 4; Length 7859; Best Local Similarity 70.6%; Pred. No. 2.38e-05; 0; Mismatches 10; Indels COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 APPLICANT: Hunter, Michael G
APPLICANT: Czaplewski, Lloyd G
TITLE OF INVENTION: Proteins and nucleic acids
NUMBER OF SEQUENCES: 73 HEBULT 6

1D US-07-854-596B-4 STANDARD; DNA; UNC; 7859 BP. Ac xxxxxx

DT 01-JAM-1900

E Sequence 4, Application US/07854596B.
CC Sequence 4, Application US/07854596B.
CC Sequence 4, Application US/07854596B.
CC SEMERAL INFORMATION:
CC PAPLICANT: Barson, Keith M. CC APPLICANT: Hunter, Michael C. APPLICANT: Caplewski, Lloyd G. TITLE OF INVENTION: Proteins and nucleic acid.
CC APLICANT: Caplewski, Lloyd G. TITLE OF INVENTION: Proteins and nucleic acid.
CC TITLE OF INVENTION: Proteins and nucleic acid.
CC APLICANT: Thicago C. CORRESPONDENCE ADDRESS:
ADDRESSEE: Dr. John J. McDonnell
CC CONNTRY: USA
CC CONTRY: USA
CC CONTRY: USA
CC CONTRY: USA
CC CONTRY: IBM PC Compatible
CC CONTRY: BPPLICANTION DATA:
CC CONTRY: DATA:
CC CONTRY: ON THE CONTRY OF ATA
CC CONTRY APPLICANTION THE
CC CONTRY APPLICANTION THE
CC CLASSIFICATION NUMBER: 26,949
CC CLASSIFICATION NUMBER: 26,949
CC TELEPRONE: 312-715-100
CT TELEPRONE: 312-715-100
CT TELEPRONE: 312-715-100
CC TELEPRONE: 312-715-100
CC STANDEDNESS: single
CC STANDEDNESS: single
CC TYPE: CLASSIFICATION INCORMATION:
CC TELEPRONE: 312-715-100
CC TTYPE: nucleic acid
CC TYPE: Nucleic acid
CC TATORNATION: 1..7859
CC LOATION: 1..7859 ADDRESSEE: Dr. John J. McDonnell STREET: Ten South Wacker Drive, Suite 3000 PCT-US93-01720-4 STANDARD; DNA; UNC; 1947 BP. 3131 GAAGTTCCTATTCTCTAGAAAGTATAGGAACTTC 3164 34 gaagttcctatacNNNNNNNNgaataggaacttc 1 24; Conservative

May 14 11:31

01-JAN-1900

APPLICANT: Druez, Catherine APPLICANT: Van Snick, Jacques TITLE OF INVENTION: Nucleic Acid Sequences Coding For TITLE OF INVENTION: Or Complementary To Nucleic Acid Sequences Coding ö Gaps ö 53.8%; Score 14; DB 9; Length 1947; 60.7%; Pred. No. 2.71e+00; 0; Mismatches 11; Indels COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage TOPOLOGY: linear Sequence 1947 BP; 379 A; 582 C; 586 G; 400 T; 0 other; IITLE OF INVENTION: Interleukin 9 Receptor APPLICATION NUMBER: PCT/US93/01720 FILING DATE: 19930225 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/847,347
FILING DATE: 09-MACH-1992
ATTORNEY/AGENT INFORMATION: APPLICANT: Renauld, Jean-Christophe APPLICANT: Druez, Catherine 1121 CCTCTACAGTGTACACAATGGGAACTTC 1148 REFERENCE/DOCKET NUMBER: LUD 264 Sequence 4, Application PC/TUS9301720. Sequence 4, Application PC/TUS9301720 GENERAL INFORMATION: 28 cctatacNNNNNNNNgaataggaacttc 1

O,

STREET: 2421 N.W. 41st Street, Suite A-1 გ APPLICANT: Van Snick, Jacques TITLE OF INVENTION: Nucleic Acid Sequences Coding For TITLE OF INVENTION: Or Complementary To Nucleic Acid Sequences Coding ö Gaps APPLICANT: Smith, Craig A.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Isolated Viral Protein TNF Antagonists
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation ö Query Match 53.8%; Score 14; DB 9; Length 1997; Best Local Similarity 60.7%; Pred. No. 2.71e+00; Matches 17; Conservative 0; Mismatches 11; Indels COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect Sequence 1997 BP; 388 A; 612 C; 593 G; 404 T; 0 other; TITLE OF INVENTION: Interleukin 9 Receptor US-08-292-549-5 STANDARD; DNA; UNC; 1065 BP. NAME: Hanson, Norman D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 264
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-8884
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHRACTERISTICS: CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/01720
FILING DATE: 19930225 APPLICATION NUMBER: US/07/847,347 FILING DATE: 09-MARCH-1992 ATTORNEY/AGENT INFORMATION: 1171 CCTCTACAGTGTACACAATGGGAACTTC 1198 28 cctatacNNNNNNNNgaataggaacttc 1 Sequence 5, Application US/08292549.
Sequence 5, Application US/08292549
Patent No. 5464938
GENERAL INFORMATION: STREET: 51 University Street = = = = ADDRESSEE: Felfe & Lynch STREET: 805 Third Avenue LENGTH: 1997 base pairs TYPE: NUCLEIC ACID STRANDEDNESS: single CORRESPONDENCE ADDRESS: PRIOR APPLICATION DATA: 17; Conservative CITY: New York City NUMBER OF SEQUENCES: TOPOLOGY: linear STATE: New York COUNTRY: USA CLASSIFICATION: ZIP: 10022 01-JAN-1900 XXXXXX RESULT

쇰 გ May 14 11:31

Washington

Partent No. 54/6781
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 54/6781el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 66
CORRESPONDENCE: David R. Saliwanchik Gaps ö Score 13; DB 4; Length 1065; Pred. No. 1.01e+01; 0; Mismatches 10; Indels Sequence 1065 BP; 327 A; 248 C; 197 G; 293 T; 0 other; SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: US-07-991-867B-41 STANDARD; DNA; UNC; 1689 BP. APPLICATION NUMBER: US/08/292,549 FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/963,330
FILING DATE: 10/19/92
ATTORNEY/AGENT INFORMATION: Sequence 41, Application US/07991867B. Sequence 41, Application US/07991867B OPERATING SYSTEM: PC-DOS/MS-DOS REFERENCE/DOCKET NUMBER: 2602-A 384 TTCCCAACAAGTGTGGAATAGGA 408 COMPUTER: IBM PC compatible NAME: Perkins, Patricia A. REGISTRATION NUMBER: 34,693 TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1065 base pairs 30 ttcctatacNNNNNNNNgaatagga 6 MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO MEDIUM TYPE: Floppy disk ORGANISM: Cowpox virus Query Match 50.0%; Best Local Similarity 60.0%; STRANDEDNESS: single TOPOLOGY: linear COMPUTER READABLE FORM: 15; Conservative TYPE: nucleic acid LOCATION: 1..1065 NAME/KEY: CDS ORIGINAL SOURCE: COUNTRY: USA ANTI-SENSE: NO 98101 01-JAN-1900 RESULT 10 XXXXXX Matches

May 14 11:31

ö Gaps ö Score 13; DB 4; Length 1947; Pred. No. 1.01e+01; 0; Mismatches 12; Indels Sequence 1947 BP; 439 A; 522 C; 609 G; 377 T; 0 other; SOFTWARE: PatentIn Release #1.0, Version #1.25 US-08-463-953-2 STANDARD; DNA; UNC; 1947 BP. CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/998, 972A
FILING DATE: 19921230
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/860, 701 REFERENCE/DOCKET NUMBER: 13952-12-2 APPLICATION NUMBER: US 07/816, 281 FILING DATE: 31-DEC-1991 ATTORNEY/AGENT INFORMATION: 1204 TCCTGTACCCGCCTGGGACAGAACTTC 1232 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS 29 tcctatacNNNNNNNNgaataggaacttc 1 REGISTRATION NUMBER: 31,990 TELECOMMUNICATION INFORMATION: TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS: FILING DATE: 31-MAR-1992 PRIOR APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk NAME: Parmelee, Steven W LENGTH: 1947 base pairs ORGANISM: Homo sapiens Query Match 50.0%; Best Local Similarity 58.6%; TYPE: nucleic acid STRANDEDNESS: single TISSUE TYPE: Hepatic 17; Conservative LOCATION: 3..1847 TOPOLOGY: linear NAME/KEY: CDS ORIGINAL SOURCE: 94105 01-JAN-1900 Matches XXXXXX RESULT 12 g

Sequence 2, Application US/08463953.
Sequence 2, Application US/08463953.
Patent No. 5502034
GENERAL INFORMATION:
APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS: STREET: One Market Plaza, Stewart Street Tower, ADDRESSEE: Townsend and Townsend Twentieth Floor STREET:

ö Gaps ö Query Match 50.0%; Score 13; DB 5; Length 1947; Best Local Similarity 58.6%; Pred. No. 1.01e+01; Matches 17; Conservative 0; Mismatches 12; Indels APPLICANT: Holly, Richard D.
APPLICANT: Foster, Donald C.
TITLE OF INVENTION: METHODS FOR PRODUCING THROMBIN
NUMBER OF SEQUENCES: 48 LOCATION: 3.1847 Sequence 1947 BP; 439 A; 522 C; 609 G; 377 T; 0 other; CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower, COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 PCT-US92-11357-2 STANDARD; DNA; UNC; 1947 BP. CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/860,701
FILING DATE: 31-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/816,281
FILING DATE: 31-DEC-1991
ATTORNEY/AGENT INFORMATION: REFERENCE/DOCKET NUMBER: 13952-12-2 TELECOMMUNICATION INFORMATION: 1204 TCCTGTACCCGCCCTGGGACAAGAACTTC 1232 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,953 Sequence 2, Application PC/TUS9211357. Sequence 2, Application PC/TUS9211357 GENERAL INFORMATION: 29 tcctatacNNNNNNNNNgaataggaacttc 1 = = --NAME: Parmelee, Steven W REGISTRATION NUMBER: 31,990 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1947 base pairs COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk TELEPHONE: 206-467-9600 TELEFAX: 415-543-5043 Twentieth Floor ORIGINAL SOURCE: ORGANISM: Homo sapiens TYPE: nucleic acid STRANDEDNESS: single TISSUE TYPE: Repatic San Francisco TOPOLOGY: linear NAME/KEY: CDS USA FILING DATE: ZIP: 94105 COUNTRY: STREET: 01-JAN-1900 g <u>ئ</u>

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CITY: San Francisco

Gaps ö BOARD OF REGENTS, THE UNIVERSITY OF Score 13; DB 8; Length 1947; Pred. No. 1.01e+01; 0; Mismatches 12; Indels COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/11357
FILING DATE: 19921230
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/860,701 LOCATION: 3..1847 Sequence 1947 BP; 439 A; 522 C; 609 G; 377 T; 0 other; COUNTRY: United States of America POSTAL CODE: 78701 PCT-US95-07439-24 STANDARD; DNA; UNC; 1947 BP. REGISTATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-12-2
TELECOMMUNICATION NUMBER: 13952-12-2
TELEPHONE: 206-467-9600
TELEPHONE: 206-467-9600
TELEPHONE: 206-467-9600
TELEPHONE: 206-467-9600
TELEPHONE: 206-467-9600
SEQUENCE: LANGERICATIOS: LENGTH: 1947 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single 201 West 7th Street Sequence 24, Application PC/TUS9507439.
Sequence 24, Application PC/TUS9507439
GENERAL INFORMATION:
APPLICANT:
APPLICANT: NAME: BOARD OF REGENTS,
APPLICANT: TEXAS SYSTEM 1204 TCCTGTACCCGCCCTGGGACAAGAACTTC 1232 APPLICATION NUMBER: US 07/816, 281 FILING DATE: 31-DEC-1991 ATTORNEY/AGENT INFORMATION: 29 tcctatacNNNNNNNNNgaataggaacttc 1 Austin COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk FILING DATE: 31-MAR-1992 PRIOR APPLICATION DATA: NAME: Parmelee, Steven W ORGANISM: Homo sapiens Query Match Best Local Similarity 58.6%; 17; Conservative TISSUE TYPE: Hepatic STREET: TOPOLOGY: linear STATE: NAME/KEY: CDS LOCATION: 3..1 USA ORIGINAL SOURCE: 94105 COUNTRY: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: 01-JAN-1900 XXXXXX RESULT 14 Matches g გ

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ö E Sequence 4, Application US/07882925A.
C Sequence 4, Application US/07882925A.
C Patent No. 5315000
C GENERAL INFORMATION:
C APPLICANT: Degen, Sandra J. F.
TITLE OF INVENTION: Gene for a growth factor and its cDNA and TITLE OF INVENTION: protein
C NUMBER OF SEQUENCES: 7
C ORRESPONDENCE ADDRESS:
C ADDRESSEE: Gregory Lunn Gaps TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF A MODIFIED TITLE OF INVENTION: EUKARYOTIC CYTOPLASMIC DNA VIRUS GENOME <u>;</u> Query Match 50.0%; Score 13; DB 4; Length 1988; Best Local Similarity 58.6%; Pred. No. 1.01e+01; Matches 17; Conservative 0; Mismatches 12; Indels CLONE: palS1-PT (Fig. 5.1) Sequence 1988 BP; 451 A; 529 C; 617 G; 391 T; 0 other; SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: STREET: Wood, Herron & Evans, 2700 Carew Tower REFERENCE/DOCKET NUMBER: 30472/106 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELERX: 899149
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS: US-07-882-925A-4 STANDARD; DNA; UNC; 2188 BP STREET: 1800 Diagonal Road, Suite 500 COUNTRY: USA
21P: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS APPLICATION NUMBER: US/07/750,080A FILING DATE: 19910826 1247 TCCTGTACCCGCCCTGGGACAAGAACTTC 1275 29 tcctatacNNNNNNNNNNaataggaacttc 1 REGISTRATION NUMBER: 29,768 ADDRESSEE: Foley & Lardner MOLECULE TYPE: DNA (genomic) APPLICANT: SCHEIFLINGER, F. NAME: BENT, Stephen A. LENGTH: 1988 base pairs APPLICANT: FALKNER, F. G. NUMBER OF SEQUENCES: 42 TYPE: NUCLEIC ACID STRANDEDNESS: single CORRESPONDENCE ADDRESS: CLASSIFICATION: 435 TOPOLOGY: linear CITY: Alexandria IMMEDIATE SOURCE: 01-JAN-1900 RESULT 16 XXXXXX გ

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Sequence 1, Application PC/TUS9305651.
Sequence 1, Application PC/TUS9305651
GENERAL INFORMATION:
ITILE OF INVENTION: A Gene Which Prevents Programmed Cell Death
NUMBER OF SEQUENCES: 5
COMPUTER READBLE FORM:
MEDIUM TYPE: diskette Gaps ö Score 13; DB 11; Length 2553; Pred. No. 1.01e+01; 0; Mismatches 12; Indels Sequence 2553 BP; 749 A; 535 C; 610 G; 659 T; 0 other; SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE FITLE OF INVENTION: CONTRACEPTIVE VACCINE RESULT 18 ID PCT-US93-05651-1 STANDARD; DNA; UNC; 6560 BP. REFERENCE/DOCKET NUMBER: 19244Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3462
TELEPHONE: (908) 594-346
ILENFRATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2553 base pairs APPLICATION NUMBER: PCT/US95/07295 APPLICATION NUMBER: PCT/US93/05651 767 AAGTIGCTCTACAGGTTCCTGAAGTGGAA 795 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS 33 aagttcctatacNNNNNNNNgaataggaa 5 ADDRESSEE: MARY A. APPOLLINA REGISTRATION NUMBER: 34,087 ATTORNEY/AGENT INFORMATION: NAME: APPOLLINA, MARY A SEQUENCE CHARACTERISTICS: LENGTH: 6560 base pairs CURRENT APPLICATION DATA: INFORMATION FOR SEQ ID NO: Query Match 50.0%; Best Local Similarity 58.6%; TYPE: nucleic acid STRANDEDNESS: double TYPE: nucleic acid STRANDEDNESS: double CORRESPONDENCE ADDRESS: 17; Conservative 17..2221 NUMBER OF SEQUENCES: MOLECULE TYPE: CDNA TOPOLOGY: linear CLASSIFICATION: NAME/KEY: CDS COUNTRY: USA ZIP: 07065 CITY: RAHWAY STATE: NJ FILING DATE: LOCATION: 01-JAN-1900 Matches XXXXXX გ

NAME/KEY: misc_feature

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Gaps ; 0 NAME/KEY: misc feature LOCATION: 408.7367 OTHER INFORMATION: /product= "Coagulation Factor VIII" Score 13; DB 10; Length 7493; RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 1 TO 7476 Sequence 7493 BP; 2487 A; 1503 C; 1436 G; 2067 T; 0 other; 0; Mismatches 11; Indels APPLICANT: Emory University TITLE OF INVENTION: Hybrid Human/Animal Factor VIII NUMBER OF SEQUENCES: 12 AUTHORS: Lakich, D. AUTHORS: Gitschier, J. ITILE: Sequence of the Murine Factor VIII cDNA. OPPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: OTHER INFORMATION: /function= "PolyA_signal" Query Match 50.0%; Score 13; DB 10; I Best Local Similarity 59.3%; Pred. No. 1.01e+01; CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Suite 2800 OTHER INFORMATION: /rpt_type= "terminal" OTHER INFORMATION: /note= "3'UTR" PCT-US94-13200-5 STANDARD; DNA; UNC; 7493 BP ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
RECISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: EMUI06CIP(2)
FELECOMMUNICATION: APPLICATION NUMBER: PCT/US94/13200 FILING DATE: 15-NOV-1994 3714 GAAGATCCTATTCCACAAGATGAAGAG 3740 Sequence 5, Application PC/TUS9413200 Sequence 5, Application PC/TUS9413200 COMPUTER: IBM PC compatible COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk TELEPHONE: 404-815-6508 NAME/KEY: repeat unit LOCATION: 7368..7493 PUBLICATION INFORMATION: 16; Conservative LOCATION: 7471..7476 Elder, F. JOURNAL: Genomics CITY: Atlanta STATE: Georgia COUNTRY: US GENERAL INFORMATION: 374-379 CLASSIFICATION: 1993 ZIP: 30309 AUTHORS: AUTHORS: AUTHORS: VOLUME: PAGES: 01-JAN-1900 FEATURE: RESULT 20 XXXXXX Matches 요 3 8888888888888888888888888888888

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Sequence 7653 BP; 2429 A; 1455 C; 1271 G; 2498 T; 0 other; Query Match 50.0%; Score 13; DB 9; Length 7653; Best Local Similarity 60.0%; Pred. No. 1.01e+01; INFORMATION FOR SEC 1D NO: 18: SEQUENCE CHARACTERISTICS: LENGTH: 7653 base pairs TYPE: nucleic acid STRANDEDNESS: double 9 tattcNNNNNNNNStataggaactt 33 MOLECULE TYPE: DNA (genomic) INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 7653 base pairs = = = = CURRENT APPLICATION DATA: CURRENT APPLICATION DATA: FILING DATE: 19930614 COMPUTER READABLE FORM: MEDIUM TYPE: diskette MEDIUM TYPE: diskette FILING DATE: 19930714 TYPE: nucleic acid STRANDEDNESS: double CITY: Cambridge STATE: Massachusetts CORRESPONDENCE ADDRESS: COMPUTER READABLE FORM: 15; Conservative OPERATING SYSTEM: linear TOPOLOGY: linear COUNTRY: U.S.A. COUNTRY: U.S.A. CLASSIFICATION: ZIP: 02139 ZIP: 02139 TOPOLOGY: COMPUTER: SOFTWARE: 01-JAN-1900 Matches RESULT PCT | 110 PCT | 120 a ð ö Gaps Sequence 1, Application PC/TUS9305705.
Sequence 1, Application PC/TUS9305705
GENERAL INFORMATION:
APPLICANT: Massachusetts Institute of Technology
TITLE OF INVENTION: Inhibitors of Ced-3 and Related Proteins
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Massachusetts Institute of Technology
STREET: 77 Massachusetts Avenue ö NAME/KEY: misc_feature
LOCATION: 408._7367
OTHER INFORMATION: /product= "Coagulation Factor VIII"
PUBLICATION INFORMATION: Query Match 50.0%; Score 13; DB 10; Length 7493; Best Local Similarity 59.3%; Pred. No. 1.01e+01; RELEVANT RESIDUES IN SEQ ID NO: 5: FROM 1 TO 7476 Sequence 7493 BP; 2487 A; 1503 C; 1436 G; 2067 T; 0 other; 0; Mismatches 11; Indels AUTHORS: Lakich, D. AUTHORS: Gitschier, J. TITLE: Sequence of the Murine Factor VIII CDNA. OTHER INFORMATION: /function= "PolyA_signal" OTHER INFORMATION: /rpt_type="terminal" OTHER INFORMATION: /note="3'UTR" OTHER INFORMATION: /rpt_type= "terminal" OTHER INFORMATION: /note= "5'UTR" PCT-US93-05705-1 STANDARD; DNA; UNC; 7653 BP. 3714 GAAGATCCTATTCCACAAGATGAAGAG 3740 34 gaagttcctatacNNNNNNNNgaatag 8 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 7493 base pairs TYPE: nucleic acid STRANDEDNESS: single MOLECULE TYPE: cDNA to mRNA HYPOTHETICAL: NO ORGANISM: Mus musculus NAME/KEY: misc feature LOCATION: 7471...7476 NAME/KEY: repeat unit LOCATION: 7368..7493 NAME/KEY: repeat_unit LOCATION: 1..407 16; Conservative AUTHORS: Elder, F. AUTHORS: Lakich, D AUTHORS: Gitschier, Genomics TOPOLOGY: linear 374-379 ORIGINAL SOURCE: ANTI-SENSE: NO VOLUME: 16 JOURNAL:

01-JAN-1900

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Matches

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APPLICANT: Massachusetts Institute of Technology TITLE OF INVENTION: Cloning and Characterization of Cell Death Genes NUMBER OF SEQUENCES: 29 ö ö MOLECULE TYPE: DNA (genomic) Sequence 7653 BP; 2429 A; 1455 C; 1271 G; 2498 T; 0 other; Query Match 50.0%; Score 13; DB 9; Length 7653; Best Local Similarity 60.0%; Pred. No. 1.01e+01; 0; Mismatches 10; Indels ADDRESSEE: Massachusetts Institute of Technology STREET: 77 Massachusetts Avenue LT 22 PCT-US93-05701-18 STANDARD; DNA; UNC; 7653 BP. APPLICATION NUMBER: PCT/US93/05705 APPLICATION NUMBER: PCT/US93/05701 Sequence 18, Application PC/TUS9305701 Sequence 18, Application PC/TUS9305701 GENERAL INFORMATION: 4399 TATICCATGAAGAGGATATGAACTT 4423 Massachusetts May 14 11:31 8888888888888888888888888888888888

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ORGANISM: Amsacta moorei entomopoxvirus complement (65..1459) MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE: 241 ATACATAACTGAGAATAGGAA 261 NAME/KEY: CDS LOCATION: 01-JAN-1900 FEATURE: XXXXXX RESULT ტ pLHDMDN-NSA: 5'LTR (position 1-1159); y+ (position 1160-1640); HisD (position 1641-2928), Myo-D NSA Apal f DESCRIPTION: (position 2929-4389); driving neo (position 4390-5259); ö Gaps Gaps ö ö ADDRESSEE: Christensen, O'Connor, Johnson and Kindness STREET: 2800 Pacific First Center, 1420 Fifth Avenue DESCRIPTION: (position 5260-5964); Figures 8A-8C. Sequence 8316 BP; 1922 A; 2246 C; 2255 G; 1880 T; 13 other; Score 13; DB 3; Length 8316; Pred. No. 1.01e+01; 8; Indels Indels TELECOMMUNICATION INFORMATION: TELEPHONE: 1-206-682-8100; 1-206-224-0727 (direct) TELEFAX: 1-206-224-0779 Patent No. 535295 GENERAL INFORMATION: APPLICANT: Tapscott, J.; Weintraub, H.M.; Palmer, T.D. TITLE OF INVENTION: "MyoD REGULATORY REGION" NUMBER OF SEQUENCES: 4 MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage COMPUTER: IBM PC/386 Compatible OPERATING SYSTEM: MS-DOS 4.01 SOFTWARE: Word for Windows-t CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/753,520B 10; US-07-753-520B-4 STANDARD; DNA; UNC; 8316 BP. Mismatches Mismatches REFERENCE/DOCKET NUMBER: FHCR-1-5789 Sequence 4, Application US/07753520B. Sequence 4, Application US/07753520B MOLECULE TYPE: Other; plasmid DNA 4399 TATTCCATGAAGAGGATATGAACTT 4423 NAME: Sundsmo, John, S. REGISTRATION NUMBER: 34,446 TELEX: 4938023
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8316 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single 9 tattcNNNNNNNNgtataggaactt 33 APPLICATION NUMBER: none FILING DATE: none ATTORNEY/AGENT INFORMATION: FILING DATE: 19910903 50.0%; 61.9%; PRIOR APPLICATION DATA: CORRESPONDENCE ADDRESS: COMPUTER READABLE FORM: 13; Conservative Conservative CLASSIFICATION: 435 CITY: Seattle STATE: Washington TOPOLOGY: linear ZIP: 98101-2347 Best Local Similarity COUNTRY: USA DESCRIPTION: DESCRIPTION: 15; 01-JAN-1900 with 3'LTR Query Match XXXXXX ragment Matches Matches RESULT

25 atacNNNNNNNNgaataggaa 5

IIILE OF INVENTION: No. 5476781el Entomopoxvirus Expression System US-07-991-867B-1 STANDARD; DNA; UNC; 8457 BP Sequence 1, Application US/07991867B
Patent No. 5476781
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E. Sequence 1, Application US/07991867B. NUMBER OF SEQUENCES:

ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: ADDRESSEE: David R. Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 APPLICATION NUMBER: US/07/991,867B FILING DATE: 12-DEC-1992 CORRESPONDENCE ADDRESS: CLASSIFICATION: 435 CITY: Gainesville STATE: FL COUNTRY: USA

NAME: Saliwanchik, David R. REGISTRATION NUMBER: 31,794 REFERENCE/DOCKET NUMBER: UF114.C3 APPLICATION NUMBER: US 07/827, 685 FILING DATE: 30-JAN-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/657,584 FILING DATE: 19-FEB-1991 ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: WO 92/14818 FILING DATE: 12-FEB-1992 INFORMATION FOR SEQ ID NO: 1: TELEPHONE: 904-375-8100 LENGTH: 8457 base pairs SEQUENCE CHARACTERISTICS: TELEFAX: 904-372-5800 TYPE: nucleic acid STRANDEDNESS: double PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: TOPOLOGY: unknown

NAME/KEY: CDS

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ö Gaps ; 0 ADDRESSEE: Christensen, O'Connor, Johnson and Kindness STREET: 2800 Pacific First Center, 1420 Fifth Avenue 50.0%; Score 13; DB 4; Length 8457; 60.0%; Pred. No. 1.01e+01; LOCATION: complement (6277..6768) Sequence 8457 BP; 3173 A; 951 C; 1006 G; 3327 T; 0 other; 0; Mismatches 10; Indels TELEPHONE: 1-206-682-8100; 1-206-224-0727 (direct) TELEFAX: 1-206-224-0779 TELEX: 4938023 Sequence 3, Application US/07753520B.
Sequence 3, Application US/07753520B
Patent No. 532595
GENERAL No. 532510:
GENERAL APPLICANT: Tapscott, J.; Weintraub, H.M.; Palmer, T.D.
TITLE OF INVENTION: "MyoD REGULATORY REGION" COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage COMFUTER: IBM PC/386 Compatible OPERATING SYSTEM: MS-DOS 4.01
SOFTWARE: Word for Windows-t CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/753,520B US-07-753-520B-3 STANDARD; DNA; UNC; 9115 BP REFERENCE/DOCKET NUMBER: FHCR-1-5789 complement (2239..2475) 7080 AAGTITCTATATATTTACACGAATA 7104 REGISTRATION NUMBER: 34,446 ELECOMMUNICATION INFORMATION: 33 aagttcctatacNNNNNNNNgaata 9 TELEX: 4938023
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS: ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: none Sundsmo, John, S. FILING DATE: 19910903 Query Match
Best Local Similarity 60.0%;
Watches 15; Conservative PRIOR APPLICATION DATA: NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS: 2502..2987 3080..6091 1474..2151 CITY: Seattle STATE: Washington FILING DATE: none ZIP: 98101-2347 CLASSIFICATION: CDS CDS CDS NAME/KEY: CDS COUNTRY: USA NAME/KEY: LOCATION: NAME/KEY: LOCATION: NAME/KEY: LOCATION: 01-JAN-1900 FEATURE: FEATURE: FEATURE: FEATURE NAME: XXXXXX RESULT 용 g 8888888888888888

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LENGTH: 9115 base pairs

MOLECULE TYPE: Other;plasmid DNA DESCRIPTION: pLHDMDN-53: 5'LTR (position 1-1159); Y+ (position DESCRIPTION: 1159-1640); HisD (position 1641-3007); Myo-D 531.4 Apal DESCRIPTION: (position 3008-5248); driving neo (position 5249-6117); DESCRIPTION: 3'LTR (position 6118-6823) coupled to a pBR322 plasmid APPLICANT: Gaertner, Frank H.

APPLICANT: Gaertner, Frank H.

TITLE OF INVENTION: No. 5468483el Bacillus thuringiensis Isolate
TITLE OF INVENTION: Having Anti-Protozoan Activity
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Roman Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STREET: 2421 N.W. 11st Street, Suite A-1
CITY: Gainesville Gaps ö DESCRIPTION: 6824-9115); Figures 7A-7D. Sequence 9115 BP; 2183 A; 2408 C; 2474 G; 2036 T; 14 other; Query Match 50.0%; Score 13; DB 3; Length 9115; Best Local Similarity 61.9%; Pred. No. 1.01e+01; 0; Mismatches 8; Indels COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/278, 685 US-08-278-685-4 STANDARD; DNA; UNC; 31 BP. REGISTRATION NUMBER: 21,023 REFERENCE/DOCKET NUMBER: 07/654,166 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/654,166
FILING DATE: 12-FEB-1991 APPLICATION NUMBER: US 08/091,527 Sequence 4, Application US/08278685. Sequence 4, Application US/08278685 Patent No. 5468483 GENERAL INFORMATION: ELECOMMUNICATION INFORMATION: FILING DATE: 12-AUG-1993 ATTORNEY/AGENT INFORMATION: NAME: Saliwanchik, Roman COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk 241 ATACATAACTGAGAATAGGAA 261 TELEPHONE: 904-375-8100 25 atacNNNNNNNNgaataggaa 5 TYPE: NUCLEIC ACID STRANDEDNESS: single 13; Conservative CLASSIFICATION: 435 TOPOLOGY: linear COUNTRY: USA FILING DATE: ZIP: 32606 01-JAN-1900 XXXXXX fragment (position Matches with a RESULT ပ္ပ ႘ පු _C 8888888

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Gaps ö Query Match 46.2%; Score 12; DB 9; Length 237; Best Local Similarity 58.3%; Pred. No. 3.58e+01; 0; Mismatches 10; Indels Sequence 237 BP; 83 A; 38 C; 52 G; 64 T; 0 other; 14; Conservative TOPOLOGY: linear Matches

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77 TAAATGAAAGGGAACAGGAACTTC 100

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APPLICANT: Irie, Reiko F
TITLE OF INVENTION: HUMAN B-LYMPHOBLASTOID CELL LINE
TITLE OF INVENTION: SECRETING ANTI-CANGLIOSIDE ANTIBODY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Poms, Smith, Lande & Rose
STREET: 2029 Century Park East, Suite 3800 CITY: Los Angeles STATE: California COUNTRY: United States of America ZIP: 90067

FILING DATE: 26-FEB-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/609803
FILING DATE: 05-NOV-1990
ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: US/08/026,320A COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS TELECOMMUNICATION INFORMATION NAME: Oldenkamp, David J REGISTRATION NUMBER: 29421 SOFTWARE: WordPerfect 5.1 REFERENCE/DOCKET NUMBER: CURRENT APPLICATION DATA: TELEPHONE: 3107885046 TELEFAX: 3102771297

INFORMATION FOR SEQ ID NO: 3: LENGTH: 360 base pairs SEQUENCE CHARACTERISTICS: STRANDEDNESS: single TOPOLOGY: linear TYPE: nucleic acid MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:

ORGANISM: Homo sapiens INDIVIDUAL ISOLATE: Epstein Barr Virus transformed B INDIVIDUAL ISOLATE: cell CELL TYPE: B-cell APPLICATION NUMBER: US 08/180,209 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy Disk 11-JAN-1994 FILING DATE: 11-MAR-1993 ATTORNEY/AGENT INFORMATION: LENGTH: 1229 base pairs CURRENT APPLICATION DATA: Query Match 46.2%; Best Local Similarity 100.0%; Matches 12; Conservative TYPE: nucleic acid STRANDEDNESS: single CORRESPONDENCE ADDRESS: MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTI-SENSE: NO FEATURE: CITY: Arlington STATE: Virginia COUNTRY: U.S.A. TOPOLOGY: linear 349 AATAGGAACTTC 360 TELEX: 133521 12 aataggaacttc 1 NAME/KEY: CDS FILING DATE: 01-JAN-1900 XXXXXX RESULT g g APPLICANT: King, Te-Piao TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED T /product= "HuMab L612 Light Chain Variable Region ö Gaps ; /function= "Immunoglobulin light Query Match 46.2%; Score 12; DB 4; Length 360; Best Local Similarity 58.3%; Pred. No. 3.58e+01; 0; Mismatches 10; Indels OTHER INFORMATION: /function= "Complementary OTHER INFORMATION: determining region 3 (CDR3)" Sequence 360 BP; 88 A; 103 C; 86 G; 83 T; 0 other; NAME/KEY: misc feature
LOCATION: 58..I08
OTHER INFORMATION: /function= "Complementary
OTHER INFORMATION: determining region 1 (CDR1)" OTHER INFORMATION: /function= "Complementary OTHER INFORMATION: determining region 2 (CDR2)" COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02629 PCT-US94-02629-54 STANDARD; DNA; UNC; 1229 BP Sequence 54, Application PC/TUS9402629. Sequence 54, Application PC/TUS9402629 GENERAL INFORMATION: STREET: 411 Hackensack Avenue ADDRESSEE: Klauber & Jackson 77 TATACAGCTCCAACAATAAGAACT 100 26 tatacNNNNNNNNgaataggaact 3 chain" FILING DATE: 10-MAR-1994 NAME/KEY: misc feature LOCATION: 154..174 NAME/KEY: misc feature LOCATION: 271..297 62 14; Conservative CORRESPONDENCE ADDRESS: PRIOR APPLICATION DATA: LOCATION: 1..360
OTHER INFORMATION: ,
OTHER INFORMATION: ,
OTHER INFORMATION: , NUMBER OF SEQUENCES: STATE: New Jersey CITY: Hackensack CELL LINE: L612 CLASSIFICATION: NAME/KEY: CDS COUNTRY: USA ZIP: 07601 01-JAN-1900 EATURE: FEATURE: EATURE: RESULT 29 XXXXXX Matches

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May 14 11:31

GENERAL INFORMATION:
APPLICANT: SHIRATORI, Toshikazu
APPLICANT: INOUE, Chihiro
APPLICANT: KITAGAMA, Yoshichika
APPLICANT: KITAGAMA, Yoshichika
APPLICANT: KITAGAMA, Toononobu
TITLE OF INVENTION: DNA FRACHENT CODING FOR MERCURIC REDUCTASE OF
TITLE OF INVENTION: THIOBACILLIDS, AND RECOMBINANT PLASMID
NUMBER OF SEQUENCES: 5 Gaps ; 0 Score 12; DB 10; Length 1229; Pred. No. 3.58e+01; 0; Indels LOCATION: 61..1056 Sequence 1229 BP; 413 A; 229 C; 261 G; 326 T; 0 other; ADDRESSEE: Nixon & Vanderhye, P.C. STREET: 1100 No. 5348888th Glebe Road, 8th Floor SOFTWARE: PatentIn Release #1.0, Version #1.25 NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 600-1-074 PCT
RELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEPHONE: 201 343-1684 Mismatches US-08-133-347-3 STANDARD; DNA; UNC; 1635 BP. PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/031,400 OPERATING SYSTEM: PC-DOS/MS-DOS Sequence 3, Application US/08133347. Sequence 3, Application US/08133347 Patent No. 5348888 COMPUTER: IBM PC Compatible INFORMATION FOR SEQ ID NO: 54: SEQUENCE CHARACTERISTICS:

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 1635 base pairs TYPE: nucleic acid STRANDEDNESS: single

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MOLECULE TYPE: CDNA TOPOLOGY: linear

CLONE: plasmid pTM314

FEATURE:

IMMEDIATE SOURCE:

ö Gaps ö APPLICANT: Drayna, Dennis T., Eaton, Dan L. TITLE OF INVENTION: No. 5474901el Plasma Carboxypeptidase Query Match 46.2%; Score 12; DB 3; Length 1635; Best Local Similarity 57.1%; Pred. No. 3.58e+01; Matches 16; Conservative 0; Mismatches 12: Indels OTHER INFORMATION: expresses T. ferrooxidans merA Sequence 1635 BP; 300 A; 517 C; 545 G; 273 T; 0 other; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible US-08-277-540-2 STANDARD; DNA; UNC; 1749 BP. ORIGINAL SOURCE: ORGANISM: T. ferrooxidans strain E-15 APPLICATION NUMBER: US/08/133,347
FILING DATE: 08-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: CRAMFORD, ARTHUR R
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 159-30 NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California APPLICATION NUMBER: US/08/277,540 FILING DATE: 19-JUL-1994 1508 TTCGTAACCGGATGACGCTACAGGAACT 1535 OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:

5 ttcctattcNNNNNNNNNStataggaact 32

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Sequence 2, Application US/08277540.
Sequence 2, Application US/08277540
Patent No. 5474901
GENERAL INFORMATION:

01-JAN-1900

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167127
FILING DATE: 15-DEC-1993
PRIOR APPLICATION DATA:

CLASSIFICATION: 435

COMPUTER READABLE FORM:

COUNTRY: USA ZIP: 94080

ORIGINAL SOURCE: ANTI-SENSE: NO

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FEATURE:

Query Match

Matches

FEATURE:

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| RESULT 33 | PCT-US9 | PC

ZIP: 20004

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Gaps 6 Query Match 46.2%; Score 12; DB 11; Length 2339; Best Local Similarity 58.3%; Pred. No. 3.58e+01; 0; Mismatches 10; Indels Sequence 222, Application US/08105483.
Sequence 222, Application US/08105483
Patent No. 5494807
GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo
TITLE OF INVENTION: SENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN MOLECULE TYPE: DNA (genomic) Sequence 2339 BP; 667 A; 469 C; 571 G; 632 T; 0 other; COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25

ö Gaps ö Query Match 46.2%; Score 12; DB 4; Length 2356; Best Local Similarity 58.3%; Pred. No. 3.58e+01; Matches 14; Conservative 0; Mismatches 10; Indels APPLICANT: Gelfand, David H.
APPLICANT: Abramson, Richard D.
TITLE OF INVENTION: 5' TO 3' EXONUCIEASE MUTATIONS OF
TITLE OF INVENTION: THERMOSTABLE DNA POLYMERASES
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cetus Corporation TOPOLOGY: linear Sequence 2356 BP; 761 A; 397 C; 340 G; 858 T; 0 other; PCT-US91-07035-11 STANDARD; DNA; UNC; 2679 BP STREET: 1400 Fifty-third Street
CITY: Emeryville
STATE: California
2IP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/07035
FILING DATE: 19910930
CLASSIFICATION: 435 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,490
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 590,466
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA: Sequence 11, Application PC/TUS9107035. FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 523, 394
FILING DATE: 15-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 143, 441
FILING DATE: 12-JAN-1988 Sequence 11, Application PC/TUS9107035 GENERAL INFORMATION: PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 063,509
FILING DATE: 17-JUN-1987 APPLICATION NUMBER: US 590,213 TELEFAX: (212) 840-0712 INFORMATION FOR SEQ ID NO: 222: SEQUENCE CHARACTERISTICS: 220 GAAATTCTTATACGTATCGGCGAA 243 34 gaagttcctatacNNNNNNNgaa 11 (212) 840-3333 LENGTH: 2356 base pairs TYPE: nucleic acid STRANDEDNESS: single PRIOR APPLICATION DATA: TELEPHONE: TELEFAX: (2 01-JAN-1900 RESULT 35 XXXXXX g 8888888888

May 14 11:31 H.P.mi

CORRESPONDENCE ADDRESS:

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ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

ö Gaps ö APPLICANT: Suzuki, Shintaro TITLE OF INVENTION: Protocadherin Materials and Methods NUMBER OF SEQUENCES: 115 Query Match 46.2%; Score 12; DB 9; Length 2757; Best Local Similarity 56.3%; Pred. No. 3.58e+01; Matches 18; Conservative 0; Mismatches 14; Indels MOLECULE TYPE: DNA (genomic) Sequence 2757 BP; 693 A; 713 C; 809 G; 542 T; 0 other; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, ADDRESSEE: Borun COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMEER: PCT/US93/06251
FILING DATE: 19930630
CLASSIFICATION: COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25 6300 Sears Tower, 233 S. Wacker Drive .r 37 PCT-US95-08071-111 STANDARD; DNA; UNC; 3033 BP. 169 AGTTCCTGTGCCTTAAGAACATTAGAACCTTC 200 Sequence 111, Application PC/TUS9508071. Sequence 111, Application PC/TUS9508071 GENERAL INFORMATION: 32 agttcctatacNNNNNNNNgaataggaacttc 1 REFERENCE/DOCKET NUMBER: 8586 400 Garden City Plaza TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 79: ATTORNEY/AGENT INFORMATION:
NAME: DiGIGLIO, Frank S.
REGISTRATION NUMBER: 31,346 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk SEQUENCE CHARACTERISTICS: LENGTH: 2757 base pairs TYPE: nucleic acid STRANDEDNESS: double CORRESPONDENCE ADDRESS: Garden City STREET: 6300 Sear CITY: Chicago STATE: Illinois COUNTRY: USA TOPOLOGY: linear STRANDEDNESS: COUNTRY: USA 90909 ZIP: 11530 01-JAN-1900 XXXXX RESULT g გ

LOCATION: 138..2528 Sequence 3033 BP; 785 A; 723 C; 723 G; 802 T; 0 other; PRIOR DATE: 23 DEC 1993

PRIOR PELICATION NUMBER: US 07/998,003

FILING DATE: 29 DEC 1992

ATTORNEY/ACENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 33,302

REFERENCE/DOCKET NUMBER: 32149

TELECOMMUNICATION INFORMATION:
TELEFAKX: 312/474-0448

TELEFAXX: 25-3856
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS: PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12588
FILING DATE: 23 DEC 1993 APPLICATION NUMBER: PCT/US95/08071 LENGTH: 3033 base pairs CURRENT APPLICATION DATA: STRANDEDNESS: single TYPE: nucleic acid MOLECULE TYPE: cDNA FEATURE: TOPOLOGY: linear CLASSIFICATION: NAME/KEY: CDS FILING DATE: May 14 11.31 88888888888888888888888888888888888

Gaps ö APPLICANT: Suzuki, Shintaro TITLE OF INVENTION: Protocadherin Materials and Methods NUMBER OF SEQUENCES: 115 0; Mismatches 11; Indels T 38 PCT-US95-08071-111 STANDARD; DNA; UNC; 3033 BP. Sequence 111, Application PC/TUS9508071. Sequence 111, Application PC/TUS9508071 GENERAL INFORMATION: 2787 TCATATTCGCTGTAACGAATTGGAAC 2812 6 tcctattcNNNNNNNNNstataggaac 31 15; Conservative 01-JAN-1900 XXXXX Matches ð

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Query Match 46.2%; Score 12; DB 11; Length 3033; Best Local Similarity 57.7%; Pred. No. 3.58e+01;

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray, & SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: STREET: 6300 Sears Tower, 233 S. Wacker Drive APPLICATION NUMBER: PCT/US95/08071 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS CORRESPONDENCE ADDRESS: CITY: Chicago STATE: Illinois COUNTRY: USA ADDRESSEE: Borun ZIP: 60606

APPLICATION NUMBER: PCT/US93/12588 FILING DATE: 23 DEC 1993

PRIOR APPLICATION DATA:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/998,003 FILING DATE: 29 DEC 1992 ATTORNEY/AGENT INFORMATION:

NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32149
TELECOMNUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEKAX: 312/474-6348
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:

LENGTH: 3033 base pairs TYPE: nucleic acid STRANDEDNESS: single

Gaps ö Query Match 46.2%; Score 12; DB 8; Length 3513; Best Local Similarity 59.1%; Pred. No. 3.58e+01; Matches 13; Conservative 0; Mismatches 9; Indels LIBRARY: LAMBDAGEM (TM) - 11 LIBRARY OF AUGUST SICK CLONE: 81F Sequence 3513 BP; 1169 A; 592 C; 769 G; 983 T; 0 other; ORGANISM: BACILLUS THURINGIENSIS PRIOR APPLICATION DATA:
APPLICATION NUMBER: 97/828,788 TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3513 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double REFERENCE/DOCKET NUMBER: MA75 NAME: SALIWANCHIK, DAVID R. REGISTRATION NUMBER: 31,794 1744 GAACTICCTATICGIGGIG 1765 MOLECULE TYPE: DNA (genomic) INDIVIDUAL ISOLATE: PS81F 1 gaagttcctattcNNNNNNN 22 ATTORNEY/AGENT INFORMATION: TOPOLOGY: linear HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: STRAIN: KENYAE IMMEDIATE SOURCE: FILING DATE: 쇰 õ

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0; Mismatches 11; Indels

2787 TCATATTCGCTGTAACGAATTGGAAC 2812

15; Conservative

Matches

Query Match 46.2%; Score 12; DB 11; Length 3033; Best Local Similarity 57.7%; Pred. No. 3.58e+01;

Sequence 3033 BP; 785 A; 723 C; 723 G; 802 T; 0 other;

LOCATION: 138..2528

NAME/KEY: CDS

MOLECULE TYPE: CDNA

TOPOLOGY: linear

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RESULT 40

PCT-US92-11337-5 STANDARD; DNA; UNC; 3513 BP.

RESULT 39 XXXXXX

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Sequence 5, Application PC/TUS9211337. Sequence 5, Application PC/TUS9211337

01-JAN-1900

Sequence 1, Application US/08278685.
Sequence 1, Application US/08278685
Patent No. 5468483
GENERAL INFORMATION:
APPLICANT: Thompson, Mark
APPLICANT: Genther, Frank H.
TITLE OF INVENTION: No. 5468483el Bacillus thuringiensis Isolate US-08-278-685-1 STANDARD; DNA; UNC; 3513 BP 01-JAN-1900 XXXXXX

GENERAL INFORMATION:
APPLICANT: PAYNE, JEMEL M.
APPLICANT: PAYNE, JESLIE A.
TITLE OF INVENTION: NOVEL BACILLUS THURINGIENSIS ISOLATES
TITLE OF INVENTION: ACTIVE AGAINST PHTHIRAPTERA PESTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:

STREET: 2421 N.W. 41st STREET, SUITE A-1

CITY: GAINESVILLE STATE: FL

COUNTRY: USA ZIP: 32606

ADDRESSEE: DAVID R. SALIWANCHIK

ADDRESSEE: Roman Saliwanchik STREET: 2421 N.W. 41st Street, Suite A-1 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: CITY: Gainesville STATE: FL

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COUNTRY: USA 2IP: 32606

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/11337

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

FILING DATE: 19921231

SOFTWARE: PatentIn Release #1.0, Version #1.25 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS CURRENT APPLICATION DATA:

888888888888888888888888888888888

REFERENCE DOCKET NUMBER: 27866/30822
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 4131 base pairs

8888888888888888888888888888888888

STRANDEDNESS: single

MOLECULE TYPE: cDNA

TOPOLOGY: linear

TYPE: NUCLEIC ACID

APPLICATION NUMBER: US 07/688,356

PRIOR APPLICATION DATA:

CLASSIFICATION: 435

May 14 11:31

FILING DATE: 04-APR-1991 ATTORNEY/AGENT INFORMATION: NAME: Noland, Greta E. REGISTRATION NUMBER: 35,302

1744 GAACTICCIAIICGIGGIGGIG 1765 Matches g δ

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Gaps ö

Query Match 46.2%; Score 12; DB 8; Length 4131; Best Local Similarity 60.0%; Pred. No. 3.58e+01; Matches 12; Conservative 0; Mismatches 8; Indels

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US-07-872-644-38 STANDARD; DNA; UNC; 4131 BP.

01-JAN-1900

XXXXXX RESULT 42

Sequence 4131 BP; 866 A; 1233 C; 1174 G; 858 T; 0 other;

148..2910

NAME/KEY: CDS LOCATION:

FEATURE:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell STREET: Two First National Plaza, 20 South Clark APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K.
TITLE OF INVENTION: DNA Encoding Mammalian
TITLE OF INVENTION: Phosphodiesterases
UDMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS: PCT-US92-03222-38 STANDARD; DNA; UNC; 4131 BP. Sequence 38, Application PC/TUS9203222. Sequence 38, Application PC/TUS9203222 APPLICANT: Beavo, Joseph A. APPLICANT: Bentley, Kelley APPLICANT: Charbonneau, Han CITY: Chicago STATE: Illinois COUNTRY: USA GENERAL INFORMATION: Street STREET: 01-JAN-1900 XXXXXX RESULT 41

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell STREET: Two First National Plaza, 20 South Clark STREET: Street SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: IITLE OF INVENTION: DNA Encoding Mammalian IITLE OF INVENTION: Phosphodiesterases APPLICATION NUMBER: US/07/872,644 2IP: 60603 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS APPLICANT: Beavo, Joseph A.
APPLICANT: Bentley, Kelley
APPLICANT: Charbonneau, Harry
APPLICANT: Sonnenburg, William K. Sequence 38, Application US/07872644 Sequence 38, Application US/07872644 Patent No. 5389527 GENERAL INFORMATION: NUMBER OF SEQUENCES: 58 CORRESPONDENCE ADDRESS: CITY: Chicago STATE: Illinois COUNTRY: USA

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19920420

COMPUTER READABLE FORM:

ZIP: 60603

May 14 11:31

May 14 11:31 FLP:mi	CC ATTORNEY/AGENT INFORMATION: CC NAMF: Heardell Lori Y		CC TELECOMMUNICATION INFORMATION:	CC TELEFAX: (213) 300-3100 CC TELEFAX: (215) 568-3439	Z		CC TYPE: nucleic acid		MOLECULE TYPE:	CC HYPOTHETICAL: NO	Seguence 4146 B	46.2%;	cal Similarity 58.3%; Pred. No. 3.58e+01;	Matches 14; Conservative U; Mismatches 10; indeis U; Gaps U;	Db 1610 TATACAAAAATAAAATGGGAACT 1633	Cp 26 tatacnnnnnngaataggaact 3	Ins	ID US-08-045-806-3 STANDARD; DNA; UNC; 5261 BP. AC xxxxxxx		DE Sequence 3, Application US/08045806.		GENERAL INFOR	APPLICANT:	CC APPLICANT: Dolwick, Kristin Marie	TITLE OF IN	TITLE OF INVENTION:		CC ADDRESSEE: Tilton. Fallon. Lungmus & Chestnut	STREET: 100		CC STATE: ILLINOIS	ZIP: 606	COMPUTER READAB!	CC COMPUTER: IBM PC compatible	SOFTWARE: Patently	CURRENT APPLICATION DATA:	APPLICATION N	CC FILING DATE: 19930408	ATTORNEY/AGENT INFO	CC NAME: Fentress, Susan B.	REGISTRATION NUMBER: 31,	CC REFERENCE/DUCKET NUMBER: NO-920/		
May 14 11.31 R.P.m. 43	CC FILING DATE: 19920420	ATA	APPLICATION NU	CC FILING DATE: U4-AFR-1991	NAME:	REGISTRATION NUMBER: 35,3	CC REFERENCE/DOCKET NUMBER: 2/866/30822	CC TELEFAX: (312) 984-9740	TELEX: . 25-3856	CC INFORMATION FOR SEQ. ID NO: 38:	CC SEQUENCE CHARACTERISTICS:		TOPOLOGY: lin	TYP	CC RAMPKEY. CDS	SQ Sequence 4131 BP; 866 A; 1233 C; 1174 G; 858 T; U other;	46.2%; Score 12; DB 3; Length 4131; larity 60.0%; Pred. No. 3.58e+01;	Matches 12; Conservative 0; Mismatches 8; Indels 0; Gaps 0;	Db 1742 TCCTATACAAGAAAGTGAAT 1761		Cp 29 tcctatacNNNNNNNgaat 10		RESULT 43		AC XXXXXX		R	CC APPLICANT: Trustees of The University of Pennsylvania	TITLE OF INVENTION: and Pathogens	NUMBER OF SEQUENCES:	CORRESPONDENCE ADDRESS:	ADDRESSE: MOGGCOCK, MASHDUIH, NUICZ, MACKIEWICZ STREET: One Liberty Place, 46th floor		COUNT		C MEDIUM TYPE: Floory disk	COMPUTER: IBM PC	OPERATING SYSTEM: PC-DOS/MS-DOS	CC SOFTWARE: Patentlin Release #1.U, Version #1.25				CC FRIOR AFFLICATION DATA: CC APPLICATION NUMBER: 08/261,822	FILING DATE: June 1

May 14 11:31 H.P.mi

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C LOCATION: 731..5272 SQ Sequence 8298 BP; 2180 A; 2086 C; 2039 G; 1993 T; 0 other; Query Match 46.2%; Score 12; DB 9; Length 8298; Best Local Similarity 59.1%; Pred. No. 3.58e+01; Matches 13; Conservative 0; Mismatches 9; Indels 0; Gaps

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1231 CAGGGGCATGAACAGGAACTTC 1252

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Search completed: Tue May 14 11:40:38 1996 Job time : 10 secs.

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Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Tue May 14 13:49:31 1996; MasPar time 32.48 Seconds 741.130 Million cell updates/sec Run on:

Tabular output not generated.

>FLP (1-34) from frt.seq 26 Description:

Perfect Score:

1 gaagttcctattcNNNNNNNNgtataggaacttc 34 N.A. Sequence:

cttcaaggataagNNNNNNNNcatatccttgaag

TABLE default Scoring table:

Gap 10

Dbase 0; Query 0 Nmatch STD 264399 seqs, 353985056 bases x 2 Searched:

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

embl-newil 1:BCT 2:FUN 3:INV1 4:INV2 5:INV3 6:MAM 7:ORG 8:PLN 9:PRII 10:PRIZ 11:PRI3 12:PRO1 13:PRO2 14:ROD 15:SYN 16:UNC 17:VRT 18:VIR

Database:

genbank91
19:BCTI 20:BCT2 21:BCT3 22:BCT4 23:BCT5 24:BCT6 25:BCT7 26:INV1 27:INV2 28:INV3 29:INV4 30:INV5 31:MAMI 32:MAM2 33:PAT1 34:PAT2 35:PAT3 36:PHG 37:PLN1 38:PLN2 39:PLN3 40:PLN4 41:PLN5 42:PLN5 43:PLN7 44:PRI1 45:RR12 46:PRI3 47:PRI4 48:PRI5 49:PRI6 50:PRI7 51:PRI8 52:PRI9 53:RDD1 54:RDD 55:RDD3 56:RDD4 57:RDD5 58:RDD7 60:STR 61:SYN 62:UNA 63:VRL1 64:VRL2 65:VRL3 66:VRL4 67:VRL5 68:VRL6 69:VRL1 70:VRT2 71:VRT3

Database:

genbank-newll 72:BCT1 73:BCT2 74:INV1 75:INV2 76:MAM 77:PHG 78:PLN 79:BCT1 80:PR12 81:PR13 82:ROD 83:STR 84:SYN 85:UNA 86:KL 87:VRT u-emb144_91

Mean 7.033; Variance 2.584; scale 2.722 Statistics:

88:part1

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Unclassified.

1 (bases 1 to 68) REFERENCE

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; 0 Snaith, M.R., Kilby, N.J. and Murray, A.H. An E. coli system for assay of FLP site-specific recombination on ö Snaith, University of Cambridge, Dept of Genetics, Downing Site, Downing Street, Cambridge CB2 3Eh, UK NCBI gi: 870842 21-JUN-1995 Submitted (16-JUN-1995) to the EMBL/GenBank/DDBJ databases. M. Gaps Gaps APDNATSR2 121 bp DNA SYN 21-JUN-19 Artificial plasmid DNA containing target site for specific ö /note="modified portion fo beta-galactosidase ö /bound_moiety="FLP site-specific recombinase" Score 26; DB 61; Length 121; Pred. No. 4.89e-08; Score 26; DB 35; Length 68; Pred. No. 4.89e-08; Indels 8; Indels beta-galactosidase; recombinase target site. .; 8 /organism="Artificial sequences" 0; Mismatches 0; Mismatches 25 gaagttcctattctctagaaagtataggaacttc 58 37 gaagttcctattctctagaaagtataggaacttc 70 Patent: WO 8703006-A 1 21-MAY-1987; 22 /note="FRT target site" /evidence=experimental /organism="unknown" Location/Qualifiers 13 g Location/Qualifiers 29 g /note="plasmid DNA" Rogers, D.T. and Szostak, J.W. recombinase (121 bp). Query Match 100.0%; Best Local Similarity 76.5%; Query Match 100.0%; Best Local Similarity 76.5%; 31 c 15 c 26; Conservative (bases 1 to 121) 2 (bases 1 to 121) 26; Conservative substrate plasmids Direct Submission 71...121 NCBI gi: 588764 1..68YEAST STRAINS unidentified. unidentified unclassified Unpublished ø æ Snaith, M. 27 misc binding misc_feature source source DEFINITION ORGANISM BASE COUNT TITLE JOURNAL BASE COUNT Matches AUTHORS JOURNAL Matches ACCESSION REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS COMMENT FEATURES FEATURES KEYWORDS TITLE COMMENT ORIGIN SOURCE ORIGIN g ð 셤 8

Snaith, M.R., Kilby, N.J. and Murray, A.H. An E. coli system for assay of FLP site-specific recombination on ö Snaith, University of Cambridge, Dept of Genetics, Downing Site, Downing Street, Cambridge CB2 3Eh, UK NCBI gi: 870843 Submitted (16-JUN-1995) to the EMBL/GenBank/DDBJ databases. M. 21-JUN-1995 21-JUN-1995 Gaps containing target site for specific APDNATSR1 154 bp DNA STYN 21-JUN-19 Artificial plasmid DNA containing target site for specific /note="5' modified portion fo beta-galactosidase" ö /note="FRT target site" /bound_moiety="FLP site-specific recombinase" Score 26; DB 61; Length 125; Pred. No. 4.89e-08; 8; Indels /translation="MEKLLFRSSYSLESIGTSSLALA" /organism="Artificial sequences" /note="pid:e; NCBI gi: 870844" /product="beta-galactosidase" H.P.rge 0; Mismatches 75 gaagttcctattctctagaaagtataggaacttc 108 1 gaagttcctattcNNNNNNNNNgtataggaacttc 34 35 /evidence=experimental Location/Qualifiers 33 g /codon_start=1 APDNATSR3 125 bp Artificial plasmid DNA recombinase (125 bp) Query Match 100.0%; Best Local Similarity 76.5%; recombinase (154 bp) 27 c (bases 1 to 125) substrate plasmids Unpublished (bases 1 to 125) 26; Conservative Direct Submission 56..>125 61..108 1..125unclassified. unidentified unidentified Snaith, M. 33 X87980 misc_feature misc_binding May 14 13:48 source DEFINITION ORGANISM DEFINITION BASE COUNT TITLE JOURNAL Matches ACCESSION REFERENCE AUTHORS AUTHORS ACCESSION JOURNAL REFERENCE CDS KEYWORDS FEATURES TITLE COMMENT RESULT SOURCE ORIGIN LOCUS LOCUS g ô

Snaith, M.R., Kilby, N.J. and Murray, A.H.
An E. coli system for assay of FLP site-specific recombination on substrate plasmids
Unpublished

(bases 1 to 154)

AUTHORS

TITLE

REFERENCE

unidentified unclassified. (bases 1 to 154)

JOURNAL REFERENCE AUTHORS Direct Submission

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Snaith, M.

beta-galactosidase; recombinase target site

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Submitted (16-JUN-1995) to the EMBL/GenBank/DDBJ databases. M.

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1 (bases 1 to 1578) Hindley, J. and Phear, G.A. Sequencing long DNA fragments cloned in bacteriophage M13 by using internal primers. The sequence analysis of a yeast DNA fragment ö SCPLA1 1019 bp DNA PLA 06-JUL-1989 Part of the 2 micron plasmid of yeast encompassing one of the Sequence of 1019 nucleotides encompassing one of the inverted repeats from the yeast 2 micrometer plasmid Nucleic Acids Res. 7 (2), 361-375 (1979) Gaps 13-JUL-1983 Saccharomyces cerevisiae Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Eumycota; Ascomycotina; Hemiascomycetes; Saccharomycetales; Saccharomycetales; Saccharomyces.

1 (bases 1 to 1019) Eumycota; Ascomycotina; Hemiascomycetes; Saccharomycetales; ; 0 Query Match 100.0%; Score 26; DB 41; Length 1019; Best Local Similarity 76.5%; Pred. No. 4.89e-08; 1 others 8; Indels SCOR01 1578 bp DNA PLN Yeast sequence containing a replication origin. V01317 /organism="Saccharomyces cerevisiae" /organism="Saccharomyces cerevisiae" 330 t 0; Mismatches /plasmid="2 micron plasmid" 192 c 225 g 330 t containing a replication origin Biochem. J. 199 (3), 819-823 (1981) 82182087 Saccharomycetaceae; Saccharomyces. Location/Qualifiers 1..1578 306 g Location/Qualifiers KST SCE.PLASMID (INCOMPL.). Hindley, J. and Phear, G.A. Saccharomyces cerevisiae origin of replication. baker's yeast. 26; Conservative 301 c inverted repeats. 1..1019terminal repeat. baker's yeast. NCBI gi: 4083 NCBI gi: 4181 271 a æ 80034481 445 V01322 DEFINITION ACCESSION KEYWORDS SOURCE DEFINITION source BASE COUNT ORIGIN sonrce BASE COUNT ORIGIN ORGANISM ORGANISM MEDLINE COMMENT AUTHORS TITLE JOURNAL MEDLINE ACCESSION JOURNAL Matches REFERENCE REFERENCE AUTHORS KEYWORDS FEATURES TITLE FEATURES COMMENT SOURCE LOCUS LOCUS 셤 ď

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/translation="MEXKITCYTTVDISQMIRKEHFEAFQSVAQCTYNQTVQLDITAF
LKTVKKANKHKFYPAFIHILARLANAHPKFRAAMKDGELVIMDSVHPCYTVFHEQTETF
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ANMDNFFAPVFTMGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMINELQQYCDEMQGG /note="SP6 RNA polymerase transcription initiation site" /note="T7 RNA polymerase transcription initiation site" /product="chloramphenicol acetyltransferase" /note="gamma replication origin from R6K" /standard_name="multiple cloning site" function="chloramphenicol resistance" /note="NCBI gi: 475711" /evidence=experimental complement (930..1589) /transl table=ll /direction=LEFT complement (174) /codon start= /gene="CmR" 399 c 112..168 430..805 1..1888 Szybalski, W. Posfai, G. 94310070 527 008461 misc_feature misc_feature misc feature misc feature rep origin source DEFINITION ORGANISM BASE COUNT Matches REFERENCE AUTHORS JOURNAL ACCESSION MEDLINE AUTHORS JOURNAL REFERENCE KEYWORDS FEATURES Ses TITLE COMMENT SOURCE ይ δ LSSHLAPAEKVSIMADAMRRIHTIDPATCPFDHQAKHRIERARTMEAGLYDQDDI.DE EHQGIAPAELFARIKARMPDGEDLVVTHGDACLPNIMVENGRFSGFIDGGRIGVADRY QDIALATRDIAEELGGEWADRFLVIJGIAAPDSQRIAFYRLI.DEFF" /translation="Miexdelhagspaawverlegydmaqoffgcsdaavfrlsaqgr pvlfvktdlsgalmelydeaarlsmlattgvpcaavldvvteagrdmlllgevpgddl ö 'note="SP6 RNA polymerase transcription initiation site" /note="T7 RNA polymerase transcription initiation site" Submitted (07-APR-1994) Gyorgy Posfai, University of Wisconsin, McArdle Laboratory for Cancer Research, 1400 University Avenue, Madison, WI 53706, USA CVPWAKK76 1814 bp DNA circular SYN 16-SEP-1994 Cloning vector pWAKK76 with kanamycin phosphotransferase (KnR) Gaps Posfai, G., Koob, M., Hradecna, Z., Hasan, N., Filutowicz, M. and In vivo excision and amplification of large segments of the ö 'note="FRT site from yeast 2 micron plasmid" /note="gamma replication origin from R6K' Indels 'product="kanamycin phosphotransferase" /standard_name="multiple cloning site" Nucleic Acids Res. 22 (12), 2392-2398 (1994) /organism="Cloning vector pMAKK76" /lab_host="Escherichia coli" ... /function="kanamycin resistance" Pred. No. 4.89e-08; 1199 gaagtteetataetttetagagaataggaaette 1232 0; Mismatches Artificial sequence; Cloning vector. 1 (bases 1 to 1814) /note="NCBI gi: 475709" /evidence=experimental complement (869..1663) /gene="KnR" 444 g Location/Qualifiers /transl_table=11 complement (174) /direction=LEF1 gene, complete sequence. /codon_start=1 Cloning vector pMAKK76. Cloning vector pMAKK76 /plasmid="" (bases 1 to 1814) Best Local Similarity 76.5%; 459 c Conservative Direct Submission 112..168430..805 Escherichia coli 1..1814NCBI gi: 475708 Szybalski, W. Posfai, G. 94310070 463 008460 26; misc_feature misc feature misc_feature misc feature rep_origin source DEFINITION ORGANISM BASE COUNT Matches JOURNAL AUTHORS ACCESSION REFERENCE AUTHORS JOURNAL MEDLINE REFERENCE CDS KEYWORDS FEATURES TITLE COMMENT SOURCE

CVPMAKC76 1888 bp DNA circular SYN 16-SEP-1994 Cloning vector pWAKC76 with chloramphenicol acetyltransferase (CmR) ö Submitted (07-APR-1994) Gyorgy Posfai, University of Wisconsin, McArdle Laboratory for Cancer Research, 1400 University Avenue, Gaps Posfai, G., Koob, M., Hradecna, Z., Hasan, N., Filutowicz, M. and In vivo excision and amplification of large segments of the ö /note="FRT site from yeast 2 micron plasmid" Indels Nucleic Acids Res. 22 (12), 2392-2398 (1994) /organism="Cloning vector pMAKC76" Pred. No. 4.89e-08; /lab host="Escherichia coli" Mismatches Artificial sequence; Cloning vector. 1 (bases 1 to 1814) 1 gaagttcctattcNNNNNNNNNgtataggaacttc 34 17 gaagttcctattctctagaaagtataggaacttc 50 Location/Qualifiers gene, complete sequence. Escherichia coli qenome Cloning vector pMAKC76. Cloning vector pMAKC76 Madison, WI 53706, USA NCBI gi: 475710 /plasmid="" (bases 1 to 1888) Best Local Similarity 76.5%; Conservative Direct Submission

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (01-JUN-1993) to the EMBL/GenBank/DDBJ databases.
Ozier-Kalogeropoullos O., CGM, CNRS, 91190 Gif sur Yvette, France
                                                                                                                                                                                                                                                                                                                         artificial sequence; cloning vectors.

1 (bases 1 to 644; 1484 to 1610; 3862 to 5807)
Yanisch-Perron,C., Vieira,J. and Messing,J.
Improved M13 phage cloning vectors and host strains: nucleotide sequences of the M13mpl8 and pUC19 vectors
Gene 33 (1), 103-119 (1985)
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                                                                                                                                                                         multicopy Saccharomyces cerevisiae/E. coli shuttle vector.
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DRMEPELMEA IPNDERDTTMPVAMATTIRKLLTGELLTLASRQQ LIDMMEADKVAGPL
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YSCTRAM2 6037 bp DNA PIN 18-JUL-1994 Cloning vector pYADE4 TRP1 and AMPr genes, complete cds. M74016 MAPr gene; TRP1 gene. pYADE4. Synthetic construct Synthetic construct; Artificial sequences.
1 (bases 1 to 6037) Brunelli,J.P. and Pall,M.L. A series of yeast shuttle vectors for expression of cDNAs and other DNA sequences Yeast 9 (12), 1299-1308 (1993) 2 (bases 1 to 6037) 2 (bases 1 to 6037) Pall,M.L. Pollin.L. Cubmitted (26-JUL-1991) Martin L. Pall, Department of Genetics and Call Biology, Washington State University, Pullman, WA 99164-4234,
/ ILLIANSELLES-TRADELER NAMELY FARE LIVANDALIA MANUALI PER SATE PER PER PER PER PER PER PER SATE MANUALI M
Length 6037;
Indels 0; Gaps 0;
CVPFL44L 6063 bp DNA SYN 15-AUG-1995 multicopy Saccharomyces cerevisiae/E. coli shuttle vector. X70484 2-micron yeast replication origin; pUC19 plasmid;

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SOURCE	cloning vectors.
ORGANISM	cloning vectors
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AUTHORS	
TITLE	Improved M13 phage cloning vectors and host strains: nucleofide sequences of the M13mp18 and pUC19 vectors
JOURNAL	Gene 33 (1), 103-119 (1985)
MEDLINE	85180545
AUTHORS	2 (bases off to 1740) Bach, M.L., Lacroute, F. and Botstein, D.
TITLE	Evidence for transcriptional regulation of orotidine-5'-phosphate
	decarboxylase in yeast by hybridization of mRNA to the yeast
TOURNAT.	structural gene cloned in Eschelland coll Proc. Natl. Acad. Sci. U.S.A. 76 (1). 386–390 (1979)
MEDLINE	9137106
REFERENCE	3 (bases 1866 to 4118)
AUTHORS	
ना।।	Trancriptional and traductional expression of a culmetic bacterial— veast plasmid in veast
JOURNAL	Gene 1, 11-19 (1980)
REFERENCE	4 (bases 1 to 6063)
AUTHORS	Ozier-Kalogeropoullos, O.
TITLE TOTIRNAL	Direct Submission Submitted (01-,IRN-1993) to the FMRI.(GenRank/DDBJ databases.
	Ozier-Kalogeropoullos O., CGM, CNRS, 91190 Gif sur Yvette, France
	e-mail:odile%FRCGM51.BITNET0vm.gmd.de
REFERENCE	5 (bases 1 to 6063)
AUTHORS	bonneaud,n., otrer-halogeropoulos,o., bl.g.i., babonesse,n., Minvielle-Sebastia.L. and Lacroute.F.
TITLE	A family of low and high copy replicative, integrative and
	single-stranded S. cerevisiae/E. coli shuttle vectors
JOURNAL	Yeast / (6), 6U9-615 (1991) 92116645
COMMENT	The pFL44L was constructed from pUC19 plasmid where two alu I sites
	were modified. The site 629 was replaced by a BqlII linker and the
	site 14) by a ciai site, ine yeast selectable marker has been closed in the Raill eite and the 2 micron 2.2 kb RooRI fragment
	containing ORI and STB gene has been cloned at the Clai site. The
	pFL44L is described in Bonneaud et al (1991): A family of low and
	high copy replicative, integrative and single-stranded S. cerevisiae/E.coli shuttle vectors. YEAST, 7 , $609-615$.
	NCBI qi: 312626
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	/organism="C
BASE COUNT ORIGIN	1607 a 1385 c 1307 g 1764 t
Query Match Best Local	100.0%; Score 26; DB 61; Length 6063; Similarity 76.5%; Pred. No. 4.89e-08;
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0b 3395 g	gaagttectataetttetagagaataggaaette 3428
Cp 34 g	HINNNNN
RESULT 17	
DEFINITION	SCA21 6318 bp DNA circular FLN 29-UUN-1993 2 micron plasmid of veast (circularly closed).
ACCESSION	V01323 J01347 L00321 L00322 L00323 L00324 M10185 M11111 M11593

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McLeod, M., Volkert, F. and Broach, J.R. Components of the site-specific recombination system encoded by the φ the protein from Escherichia coli cells expressing the cloned FLP The FLP recombinase of the Saccharomyces cerevisiae 2-micron plasmid attaches covalently to DNA via a phosphotyrosyl linkage Mol. Cell. Biol. 5, 3274-3279 (1985) The FLP protein of the 2-micron plasmid of yeast: Purification Sequence of 1019 nucleotides encompassing one of the inverted Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Endomycetales; Signals for transcription initiation and termination in the Gronostajski, R.M. and Sadowski, P.D.
Determination of DNA sequences essential for FLP-mediated recombination by a novel method
J. Biol. Chem. 260, 12320-12327 (1985) Recombination within the yeast plasmid 2-micron circle is Andrews, B.J., Proteau, G.A., Beatty, L.C. and Sadowski, P.D. The FLP recombinase of the 2 micron circle DNA of yeast: Babineau, D., Vetter, D., Andrews, B.J., Gronostajski, R.M., Cold Spring Harb. Symp. Quant. Biol. 49, 779-787 (1984) 85153059 Senecoff, J.F., Bruckner, R.C. and Cox, M.M.
The FLP recombinase of the yeast 2-micron-m plasmid: Characterization of its recombination site
Proc. Natl. Acad. Sci. U.S.A. 82, 7270-7274 (1985)
86042647 Saccharomyces cerevisiae plasmid 2 micron circle Mol. Cell. Biol. 5, 2770-2780 (1985) Proteau, G.A., Beatty, L.G. and Sadowski, P.D. Broach, J.R., Guarascio, V.R. and Jayaram, M. Hartley, J.L. and Donelson, J.E. Nucleotide sequence of the yeast plasmid Nature 286, 860-865 (1980) repeats from the yeast 2 micron plasmid J. Biol. Chem. 260, 12313-12319 (1985) 86008307 Interaction with its target sequences Cell 40, 795-803 (1985) Nucleic Acids Res. 7, 361-375 (1979) Gronostajski, R.M. and Sadowski, P.D. (bases 1 to 6318; 1 to 6318) yeast plasmid 2-micron circle Sutton, A. and Broach, J.R. Hindley, J. and Phear, G.A. Saccharomyces cerevisiae 6 (bases 5570 to 5605) Cell 29, 227-234 (1982) 4 (bases 3881 to 4020) 3 (bases 3891 to 3990) 10 (bases 667 to 739) 5 (bases 670 to 732) (bases 1 to 1022) Saccharomycetaceae. site-specific (sites) 8 (sites) 9 (sites) 82259368 81012161 85176933 6008308 86284639 86310798 80034481 ORGANISM AUTHORS TITLE AUTHORS AUTHORS MEDLINE AUTHORS MEDLINE AUTHORS AUTHORS AUTHORS JOURNAL AUTHORS AUTHORS MEDLINE MEDLINE REFERENCE MEDLINE REFERENCE JOURNAL REFERENCE JOURNAL REFERENCE JOURNAL REFERENCE REFERENCE JOURNAL MEDLINE REFERENCE MEDLINE JOURNAL MEDLINE REFERENCE JOURNAL JOURNAL JOURNAL JOURNAL REFERENCE TITLE TITLE TITLE TITLE TITLE TITLE

 (sites)	Inchedition of the crossover site during FLP-mediated Identification of the crossover site during FLP-mediated recombination in the Saccharomyces cerevisiae plasmid 2 microircle Mol. Cell. Biol. 6, 3357-3367 (1986)	sites; FIP cleavage. sites; FIP cleavage. sites; FIP cleavage. learn copy sequence for [5] kindly provided by J.S. start of the companies two 599 bp inverted regarated by a large unique (UL) and a small unique (US) start of micron plasmid contains two 599 bp inverted regarated by a large unique (UL) and small unique (US) start of micron plasmid contains two 599 bp inverted regarated by a large unique (UL) and a small unique (US) ing recombination the UI and US regions invert producence forms that differ in the orientation of one unity to the other. The A form is presented below. y 2-micron circle-encoded protein needed for specify obbination between the TRs of 2-micron circle. The the recombination site required for efficient FIP obbination site of two 13 bp inverted repeats (post-102 and 711-723) and all of an B bp spacer (703-710 recombinase cleaves the DNA at the boundaries of the recombinase cleaves the DNA at the boundaries of the recombination is reduced if the space onbinant site is increased or decreased by 1 bp, which in the second site is unaltered [5]. Recombination in the second site is unaltered [5]. Recombination of the space regions is important in FIP-promoted recombination for the sites site is increased or decreased by the recombinate spacer region. Another 13 bp direct repeat, is four itions 676-688 [5]. FIP-mediated recombination investes that are inverted with respect to each other restsion of the DNA sequences between the sites [4]. ticipating recombination sites are in direct orient motes only the excision of the intervening DNA sequences between the sites [4]. ticipating recombination sites are in direct orient and the 'ady codon (postion 2008) at positions 20 plete source information: start codon in phase with the Repl coding region is 3 ittions 1966-1964. Two CAP sites for Repl mRNA are lond formation: start codon in phase with the Repl coding region is 3 ittions 1966-1964. Two CAP sites for Repl mRNA are lond formation: start codon (postion 2008) at positions cource informa	NCBI gi:	/ Organism="Saccharomyces cerevisiae" 1545
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replace(561,"") /citation=[1]	replace((622.624)(622.624),**)	/CICALION=[1] replace(642,"")	/citation= l replace((65.666)(665.666),"")	/citation=[1] 673722	/note="FLP recombinase binding site A [9]" /hound moietv="FLP recombinase"	replace((193.794)(193.794),"")	/citation=[1] complement(8362038)	/note="Repl mRNA (alt.)"	complement(8352017) /note="Repl mRNA (alt.)"	complement (836.2019)	/note="Repl mRNA (alt.)" complement(8362010)	/note="Repl mRNA (alt.)"	3362	/note="Repl mRNA (alt.)"	Comprement(030:.2003) /note="Repl mRNA (alt.)"	(800)	/note="Kep 1 protein; Nubl gi: 1/2192" /codon start=1	/translation="MNGERLLACIKQCIMQHFQPMVYDESRCVIETTRGTFPVPDNYK	KYKTLAFAFVGHVLNTDDTPVIEKELDMPDPALVYNTIVDRIINHPELSQFISVAFIS OIKATIGEGIDINVKGTINBRGKGIRBPKRVFFBYMFSDFVNTKVTAFFSYIRDYNKI	ASEYHNITKI ILTFSCQAYMASGPNFSALKNVIRCS I IHEY ISKFVEREQDKGHIGDQ	ELPPEEDPSRELMNVQHEVNSLTEQDAEADECIMGEIDSICEKMQSEAEDQTEAEIIA	DKI I GNOKKMANIALIKKIDE KAVILIHI INELIKOGOTVAVI KGOOFOHDOLNISLHIE EQHITAVWVYLTVKFEEHWKPVDVEVEFRCKFKERKVDG"	22542841	/note="D mRNA (alt.; 5' end +/- 3 bp)" 22542861	/note="D mRNA (alt.; 5' end +/- 3 bp)"	22712816 /mcfn="D mattein: NCBI di: 172103"	processi; art=1	/translation="MPYKTAIDCIEELATQCFLSKLTDDDVSTFRRVCSKENDIIKLA	LRIPRTIDYTSILRLLYDTLPLRSLSFNEALPLFCYSIDPAQQRQCDLRFYLRDVVKL addrest former it on the self sentence in the self sent	INFERPALÇOYPETOSIFEPV"		/note="IKL" ng 39303979	-	/bound_moiety="FLP recombinase"	complement(41083182) /note="REP2 mRNA (major alt.)"	5183)	/note="REP2 mRNA (major alt.)"	complement(41083184) /note="REP2 mRNA (major alt.)"	41085223)	/note="REP2 mRNA (minor alt.)"	complement(41085195) /note="REP2 mRNA (major alt.)"
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Note: remainder of annotations omitted.

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85176933
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                                                                                                                                                                                                                                                                                                                                                                                                   McLeod, M., Volkert, F. and Broach, J.R. Components of the site-specific recombination system encoded by the yeast plasmid 2-micron circle Cold Spring Harb. Symp. Quant. Biol. 49, 779-787 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Broach, J.R., Guarascio, V.R. and Jayaram, M. Recombination within the yeast plasmid 2-micron circle is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hartley, J.L. and Donelson, J.E. Nucleotide sequence of the yeast plasmid Nature 286, 860-865 (1980)
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                Gronostajski, R.M. and Sadowski, P.D.
                                                                                                                                                                            Babineau, D., Vetter, D., Andrews, B.J., Gronostajski, R.M., Proteau, G.A., Beatty, L.G. and Sadowski, P.D.
                                                                                                                                                                                                                                                                                      Andrews, B.J., Proteau, G.A., Beatty, L.G. and Sadowski, P.D. The FLP recombinase of the 2 micron circle DNA of yeast: Interaction with its target sequences
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Determination of DNA sequences essential for FLP-mediated
                                                                                                                gene
                                                                                                                                 The FLP protein of the 2-micron plasmid of yeast: Purification of the protein from Escherichia coli cells expressing the cloned FLP
                                                                                                                                                                                                                                                                                                                                                                                   85153059
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                                                                     6008307
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                                               (sites)
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Pred. No. 4.89e-08;
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positions 6/6-888 [5]. FLP-mediated recombination involving two FLP sites that are inverted with respect to each other results in inversion of the DNA sequences between the sites [4]. If the participating recombination sites are in direct orientation, FLP promotes only the excision of the intervening DNA sequences [4]. The Rep I and Rep proteins are involved plasmid partitioning and protein stability. A start codon in phase with the Repl coding region is located at	
relatively unaffected, suggesting that pairing of sequences in spacer regions is important in FLP-promoted recombination events [5]. The sequence asymmetry utilized by the recombinase to determine the orientation of the site is located uniquely within the spacer region. Another 13 bp direct repeat, is found at	
pecomes covalently linked to the spacet way [3], [7]. The efficiency of the recombination is reduced if the spacer in a recombinant site is increased or decreased by 1 bp, while the spacer in the second site is unaltered [5]. Recombination between two sites with identical 1-base pair additions or deletions is	
ch)-70;	
relative to the other. The A form is presented below. FLP is the only 2-micron circle-encoded protein needed for specific site recombination between the IRs of 2-micron circle. The minimal siz of the recombination site required for efficient FLP	
Yeast 2 micron plasmid contains two 599 bp inverted repeats separated by a large unique (UL) and a small unique (US) region. During recombination the UL and US regions invert producing two sequence forms that differ in the orientation of one unique region	
 (7) sites; FLP cleavage. (11) sites; FLP-mediated recombination crossover site. Draft entiand clean copy sequence for [5] kindly provided by J.Senecoff, 24-JAN-1986. 	
Mol. Cell. Biol. 6, 3357-3367 (1986) 87089667 [8] sites; mRNA CAP sites and poly-adenylation sites. [9] sites;	JOURNAL MEDLINE COMMENT
nc.ecu,n., vialt,3. and produl,v.n. Identification of the crossover site during FLP-mediated recombination in the Saccharomyces cerevisiae plasmid 2 micron circle	TITLE
Graft C and Proach 1 B	MEDLINE
Senecoff, J.F., Bruckner, R.C. and Cox, M.M. The FLP recombinase of the yeast 2-micron-m plasmid: Characterization of its recombination site Characterization of its recombination site Drop Mat 1 Acad Sci 11 CA 80 7770-7774 (1984)	AUTHORS TITLE
plasmid access covalency to MMA via a phosphocytosyl illnage Mol. Cell. Biol. 5, 3274-3279 (1985) 8310798 10 (bases 667 to 739)	JOURNAL MEDLINE REFERENCE
	REFERENCE AUTHORS TITLE
Saccharomyces cerevisiae plasmid / micron circle Mol. Cell. Biol. 5, 2770-2780 (1985) 86284639	JOURNAL MEDLINE
8 (sites) 8 (sites) Sutton, A. and Broach, J.R. Signals for transcription initiation and termination in the	REFERENCE AUTHORS TITLE
recombination by a novel method J. Biol. Chem. 260, 12320-12327 (1985) 86008308	JOURNAL MEDLINE

Complete source information: positions 1966-1964. beyond the 'atg' code

codon

Two CAP sites for Repl mRNA are located (position 2008) at positions

2004 and

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FEATURES
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                                                                                                                                                                                                                                                                                                   translation="mngerllacikgcimgheqpmvydesrcviettrgtfpvpDnyk/
| KYKTLAFAFvGHVLNTDDTPVIEKELDMPDPALVYNTIVDRIINHPELSQFISVAFIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /bound_moiety="FLP recombinase" replace((793.794)..(793.794),"")
                                      /note=*D protein; NCBI gi: 172193*
                                                                                                                                                                                       EQHITAVWYYLTVKFEEHWKPVDVEVEFRCKFKERKVDG
                                                                                                                                                                                                              DRIIGNSQRMANLKIRRTKFKSVLYHILKELIQSQGTVKVYRGSSFSHDSIKISLHYE
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transTation="MPYKTAIDCIEELATQCFLSKLTDDDVSTFRRVCSKENDIIKLA/
                                                                                       /note="D mRNA (alt.; 5'
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                       /codon_start=1
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Hartley, J.L. and Donelson, J.E.
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                                            /translation="MNGERLIACIKQCIMQHFQPMVYDESRCVIETTRGTFPVPDNYK
KYKTLAFAFVGHVLNTDDTPVIEKELDMPDPALVYNTIVDRIIMHPELSQFISVAFIS
QLKATIGEGLDINVKGTLNRRGKGIRRPKGVFFRYMESPFVNTKVTAFFSYLRDYNKI
ASEYHNNTKFILTFSCQAYMASGPNFSALKNVIRCSIIHEYISKFVEREQDKGHIGDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="REP2 mRNA (major alt.)"
complement(4108..5184)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (4108..5195)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="REP2 mRNA (major alt.)"
complement (4108..5223)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (4108..5183)
DRIIGNSQRMANLKIRRTKFKSVLYHILKELIQSQGTVKVYRGSSFSHDSIKISLHYE
                        ELPPEEDPSREINNVQHEVNSLTEQDAEADEGIMGEIDSICEKMQSEAEDQTEAEIIA
                                                                                                                                                                                                                   complement (887..2008)
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                                                                                                                                         /product="protein Baker"
                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                          /note="NCBI gi: 4183"
                                                                                                                                                                                                                                         /plasmid="2 micron plasmid"
                                                                                                                                                                                                                                                                 /organism="Saccharomyces cerevisiae"
                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="REP2 mRNA (major alt.)"
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Pred. No. 4.89e-08;
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Local Similarity 76.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cloning vector sequence (E. coli/yeast/phage P1) ADH2 gene, promoter; beta-lactamase gene; TRP1 gene; CYC1 gene, terminator;
                                                                                                                                                                                                                                                                                           Submitted (07-JUN-1993) Martin L. Pall, Department of Genetics and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brunelli, J.P. and Pall, M.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brunelli, J.P. and Pall, M.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cloning vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYNECOYST
                                                                                                                                                                                                                                                                     Cell Biology, Washington State University, Pullman, WA 99164-4234,
                                                                                                                                                                                                                                                                                                              Direct Submission
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94205260
                                                                                                                                                                                                                                                                                                                                                                                                          plasmid excision
                                                                                                                                                                                                                                                                                                                                                                                                                        designed for directional cloning of cDNAs and cre/lox-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                             A series of yeast/Escherichia coli lambda expression vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA sequences
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                                      /gene="ADH2"
750..1500
1799..2889
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NGMLSSQEASQAA I DLMLQNNKLLDNRKQLYKS I A I I I GRLPEKDKKRATEMLMRKMD
                                                                                               81..668
                                                                                                                                                                                                1..6445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="NCBI gi: 4184"
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                     /note="beta-lactamase"
                                                                                                                 /standard_name="polylinker"
                                                                                                                                                  'sequenced_mol="DNA"
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Pred. No. 4.89e-08;
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STATE TO THE TENT OF THE TENT Ъ BASE COUNT Query Match Best Local S Matches LT 22 CV37458 5068 gaagttcctatactttctagagaataggaacttc 5101 10-NOV-1995 (Rel. 45, Last updated, Version 1)
Yeast CUP1 expression-multicopy (2micron) cloning vector YRTAG300
with the hemagglutinin tag sequence, complete sequence. selection). 10-NOV-1995 10-NOV-1995 misc_feature misc_feature rep_origin Sequence 6624 BP; 1845 A; 1543 C; 1397 G; 1839 T; 0 other; misc_feature source U37458; terminator ě NCBI gi: 1052969 Benjamin Lieberman, Pharmacology, Duke University, Research Drive, P.O. 3813, Durham, NC 27710, USA Lieberman B.; Endomycetales; Saccharomycetaceae. Eukaryota; Saccharomyces cerevisiae (yeast) Submitted (03-OCT-1995) to the EMBL/GenBank/DDBJ databases. -6624 34 gaagttcctatacNNNNNNNngaataggaacttc 1 Similarity 76.5%; 26; /standard_name="CYC1 terminator" 1790 a 1354 c 1443 g 1858 t Plantae; Thallobionta; Eumycota; Hemiascomycetes; standard; circular DNA; FUN; 6624 (Rel. Conservative /organism="Saccharomyces cerevisiae" /note="based on pRS424 (TRP selection); includes CUPl promoter, Cyc terminator and the hemagglutinin coding 3040.. 5880..6420 5785..5850 5660..5745 /transl_table=11
/product='N-(5'-phosphoribosyl)-anthranilate isomerase*
/note=*pid:g1052971* /gene="TRP1" complement (4514..5215) 574..1434 region fused in frame to a start codon and and two restriction sites (SstI and XhoI)" 3790..5465 /codon_start=l /note=*HA TAG with start codon /product="beta-lactamase" transl_table=11/ /note="NCBI gi: 1052970" Location/Qualifiers /note="lox site" /note="lox site" /note="TRP1 /note="NCBI gi: 1052971" note="pid:g1052970" codon start= /note="2 micron origin" 45, Created) 100.0%; . 3098 gene" Score 26; DB 61; Pred. No. 4.89e-08; ; Mismatches DB 61; Length 6445; В₽ œ. (EcoRI-HATAG-SSTI-XHOI) Indels 0; Gaps 0

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6070 gaagtteetattetetagaaagtataggaaette 6103

1 gaagttcctattcNNNNNNNgtataggaacttc 34

Matches

Local

Similarity 26;

100.0%;

Pred. No. 4.89e-08; Score 26; <u>.</u>

DB 2;

Length 6624;

Mismatches

Indels

9 Gaps

<u>,</u>

Conservative

COMMENT

NCBI gi:

1052969

ocation/Qualifiers

FEATURES

source

Sg

transl table=11/ /codon start=1 /note="NCBI gi: 1052970"

/product="beta-lactamase"

promoter, Cyc terminator and the hemagglutinin coding region fused in frame to a start codon and and two

/organism="Saccharomyces cerevisiae" /note="based on pRS424 (TRP selection); includes CUP1

restriction sites (SstI and XhoI)"

SOURCE KEYWORDS

ORGANISM

Cloning vector YRTAG300 Cloning vector YRTAG300

artificial sequence; cloning vectors.

DEFINITION ACCESSION

U37458

Yeast CUP1 expression-multicopy (2micron) cloning vector YRTAG300

with the hemagglutinin tag sequence, complete sequence. selection).

23

CVU37458

6624 bp

DNA

circular SYN

08-NOV-1995

REFERENCE

TITLE

Direct Submission

JOURNAL

Submitted (03-OCT-1995) Benjamin Lieberman, Pharmacology, Duke University, Research Drive, P.O. 3813, Durham, NC 27710, USA

AUTHORS

Lieberman, B.

(bases 1 to 6624)

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Best Local Similarity 76.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (11-NOV-1993) David J. Stillman, Dept. of Cellular, Viral and Molecular Biology, University of Utah Medical Center, Salt Lake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sikorski, R.S. and Hieter, P. A system of shuttle vectors and yeast host strains designed for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cloning vector pRS425
                 ENTRY YEP 24
                                                  Gilbert under the auspices of the GenBank Currator
                                                                  These data and their annotation were supplied to GenBank by Will
                                                                                Unpublished
                                                                                                     Obtained from VecBase 3.0
                                                                                                                       Gilbert, W.
                                                                                                                                                     Artificial sequences
                                                                                                                                                                                        Synthetic construct DNA.
                                                                                                                                                                                                                       YEp24 yeast extrachromosomal L09156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Christianson, T.W., Sikorski, R.S., Dante, M., Shero, J.H. and
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1 (bases 1 to 6849)
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TITLE YEp24 - Yeast Extrachromosomal plasmid
                               Yeast Extrachromosomal plasmid
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Pred. No. 4.89e-08;
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ORIGIN BASE COUNT

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1543 c

1397 g

1839 t

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GELLDWNS I SDWVGRQESPES LHFMLAGGLTPENVGDALRLNGVI GVDVSGGVETNGV IDIVQLHGDESWQEYQEF1GLPVIKRLVFPKDCNILLSAASQKPHSFIPLFDSEAGGT LGI I CVPNRKRT I DPV I ARK I SSLVKA YKNSSGT PKY LVGVFRNOPKEDVLALVND YG translation="MKHTKAAWSMSVINFTGSSGPLVKVCGLQSTEAAECALDSDADL/ /product="N-(5'-phosphoribosyl)-anthranilate isomerase" SG

/codon_start=1
/transl_table=11

/note="NCBI gi: 1052971" complement (4514..5215) misc_feature

3040..3098

/note="HA TAG with start codon (EcoRI-HATAG-SSTI-XHOI)"

DRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQQLIDWMEADKVAGPL

RSALPAGWF IADKSGAGERGSRGI IAALGPDGKPSR IVVI YTTGSQATMDERNRQ IA

IELDIAVSGK I LESFRPEERFPMMSTFKVLLCGAVLSR I DAGQEQLGRR I HYSQNDLVE /SPVTEKHLTDGMTVRELCSAA I TMSDNTAAN LLLTT I GGPKELTAF LHNMGDHVTRL

translation="MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY

Query Match

Best Local

Similarity

100.0%; llarity 76.5%; Conservative

Score 26; DB 84; 1 Pred. No. 4.89e-08; 0; Mismatches 8:

Length 6624; Indels

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0

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23

May 14 13:48

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REFERENCE REFERENCE REFERENCE SDOOT REFERENCE SOURCE KEYWORDS DEFINITION REFERENCE ACCESSION TITLE AUTHORS TITLE TITLE TITLE AUTHORS MEDLINE AUTHORS ORGANISM JOURNAL JOURNAL JOURNAL MEDLINE JOURNAL AUTHORS JOURNAL AUTHORS 26 The pFI46L was constructed from pUC19 plasmid where two alu I sites were modified. The site 629 was replaced by a BglII linker and the site 747 by a ClaI site. The yeast selectable marker has been cloned in the BglII site and the 2 micron 2.2 kb EcoRI fragment A family of low and high copy replicative, integrative and single-stranded S. cerevisiae/E. coli shuttle vectors Yanisch-Perron,C., Vieira,J. and Messing,J. Improved M13 phage cloning vectors and host strains: nucleotide sequences of the M13mp18 and pUC19 vectors cloning vectors multicopy Saccharomyces cerevisiae/E. coli shuttle vector. high copy replicative, integrative and single-stranded containing ORI and STB gene has been cloned at the ClaI site. The Minvielle-Sebastia, L. and Lacroute, F. Bonneaud, N., Ozier-Kalogeropoullos O., CGM, CNRS, 91190 Gif sur Yvette, France Submitted (01-JUN-1993) to the EMBL/GenBank/DDBJ databases Direct Submission Ozier-Kalogeropoullos,O. Chevalier, M.R. and Lacroute, F.
Trancriptional and traductional expression of a chimeric Proc. Natl. Acad. Sci. U.S.A. 76 (3), 1035-1039 (1979) hybrid DNA molecules High-frequency transformation of yeast: autonomous replication of Struhl, K., Stinchcomb, D.T., Scherer, S. and Davis, R.W. artificial sequence; cloning vectors.

1 (bases 1 to 644; 3499 to 3625; 5877 to 7822) cloning vectors. pUC19 plasmid. 2-micron yeast replication origin; LEU2 selectable marker; X70269 CVPFL46L pFL46L is described in Bonneaud et al (1991): 'A family of low and Yeast 7 (6), 609-615 (1991) e-mail:odile%FRCGM51.BITNET@vm.gmd.de Gene 1, 11-19 (1980) bacterial- yeast plasmid in yeast 85180545 Gene 33 (1), 103-119 (1985) 79180126 (bases 1 to 7822) (bases 3625 to 5877) (bases 644 to 3499) (bases 1 to 7822) Ozier-Kalogeropoulos, O., Li, G.Y., Labouesse, M., 7822 bp 15-AUG-1995

S gaagttcctattcNNNNNNNgtataggaacttc 34

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밁 BASE COUNT FEATURES Query Match Best Local Similarity Matches 5154 gaagtteetataetttetagagaataggaaette 5187 source S.cerevisiae/E.coli shuttle vectors'. YEAST, 7, 609-615 NCBI gi: 397134 26; 2222 a /organism="Cloning 1 1664 c 1691 g 1..7822 Location/Qualifiers 100.0%; Score 26; DB 61; Pred. No. 4.89e-08; **;** Mismatches y vector* 1 2245 t Length 7822; œ Indels 0 Gaps 0

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CV33753
U33753;
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Sequence 7834 BP; 2192 A; 1672 C; 1646 G; 2324 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (10-AUG-1995) to the EMBL/GenBank/DDBJ databases. David J. Stillman, Division of Molecular Biology and Genetics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stillman D.J.;
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Proc. Natl. Acad. Sci. U.S.A. 86:3599-3603(1989).
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Colicelli J., Birchmeier C., Michaeli T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wigler M.;
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                                                                                     artificial sequence; cloning vectors.

1 (bases 1 to 7834)

Colicelli,J., Birchmeier,C., Michaeli,T., O'Neill,K., Riggs,M.
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high-affinity cAMP phosphodiesterase
                                                                 Wigler, M.
                                                                                                                                                                                                                    cloning vectors.
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                               Isolation and characterization of a mammalian
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nq vector pADNS, with ADH1 promoter, complete
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Pred. No. 4.89e-08;

 Mismatches

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Best Local Similarity 76.5%;
Matches 26; Conservative
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Sequence 4 from patent US 5434073. I13185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (10-AUG-1995) David J. Stillman, Division of Molecular Biology and Genetics, Department of Oncological Sciences,
                             113185
                                                                                                                                                                                                                                                                           NCBI gi: 512887
                                                                                                                                                                                                                                                                                                                                                              unclassified
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Pred. No. 4.89e-08;
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Pred. No. 4.89e-08;
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A19996 standard; DNA; SYN; 7859 BP.
A19996;
14-UUL-1995 (Rel. 44, Created)
14-UUL-1995 (Rel. 44, Last updated, Version 1)
SEQ ID NO: 4; Synthetic plasmid pSW6.
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Patent number WO9109125-A/4, 27-JUN-1991.
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 PHARMACEUTICALLY ACTIVE PROTEINS COMPRISING AN ACTIVE PROTEIN AND
                                                                 unidentified
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BP; 2317 A; 1656 C; 1600 G; 2286 T; 0 other;
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SOURCE S May 14 13:48 REFERENCE FEATURES COMMENT REFERENCE KEYWORDS ACCESSION DEFINITION BASE COUNT FEATURES COMMENT Query Match Best Local S TITLE AUTHORS ORGANISM AUTHORS Matches JOURNAL JOURNAL JOURNAL CDS 3131 gaagttcctattctctagaaagtataggaacttc 3164 source rep_origin source 1 gaagttcctattcNNNNNNNgtataggaacttc 34 ယ္ယ Cloning vector pACT2 Submitted (21-JUN-1995) John S. Stile, Clontech Laboratories, Inc., 4030 Fabian Way, Palo Alto, CA 94303, USA
This vector can be obtained from CLONTECH Laboratories, Inc., 4030 CVU29899 8117 bp DNA circular SYN 01-Cloning vector pACT2 MatchmakerII, complete sequence. 3 or E-mail TECH@CLONTECH.COM. an error in this sequence, please contact CIONTECH's Technical Service Department at (415) 424-8222 or (800) 662-2566, extens customers, please contact your local distributor. For technical information, call (415) 424-8222 or (800) 662-2566, extension 3. This sequence has been compiled from information in the sequence databases, published literature and other sources, together with Fabian Way, Palo Alto, CA 94303, USA. To place an order call (415) 424-8222 or (800) 662-2566, extension 1. International Direct Submission Stile, J.S. Unpublished Clontech Vectors On Disk, Kitts, P.A. artificial sequence; cloning vectors.
1 (bases 1 to 8117) Cloning vector pACT2 U29899 NCBI gi: 513171 Patent: WO 9207874-A 33 14-MAY-1992; NCBI gi: 915409 partial sequences obtained by CLONTECH. If you suspect there is h 100.0%; Similarity 76.5%; AN INTEGRINAFFINITY SEQUENCE 26; (bases 1 to 8117) /lab host="yeast expression vector pSW6" $2345 \text{ a} \quad 1\overline{69}5 \text{ c} \quad 1638 \text{ g} \quad 2306 \text{ t}$ Conservative /trans\(\bar{1}\) table=11
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/translation="MSAPKKIVVLPGDHVGQEITAEAIKVLKAISDVRSNVKFDFENH
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YANLRPCNFASDSLLDLSPIKPQFAKGTDFVVVRELVGGIYFGKRKEDDGDGVAMDSE 1..2057 1..7984 /note="NCBI gi: 915410" 2474..3568 1..8117 Location/Qualifiers /codon_start=1 /note="Yeast 2 micron ori" organism="Cloning vector pACT2" Location/Qualifiers organism="Artificial sequences" Score 26; DB 34; Length 7984; Pred. No. 4.89e-08; 0; Mismatches version 1.3 FLP rge Indels 01-AUG-1995 <u>.</u> Gaps extension <u>.</u>

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33 SQ FITTER misc_feature S S S misc_feature misc_feature promoter SG published literature and other sources, together with partial sequences obtained by CLONTECH. If you suspect there is an error this sequence, please contact CLONTECH's Technical Service Department at (415) 424-8222 or (800) 662-2566, extension 3 or This vector can be obtained from CLONTECH Laboratories, Inc., 4030 Fabian Way, Palo Alto, CA 94303, USA. To place an order call (415) 424-8222 or (800) 662-2566, extension 1. International customers, Sequence 8393 BP; rep_origin terminator rep_origin source æy Alto, CA 94303, USA Stile J.S.; rep_origin has been compiled from information in the sequence databases call (415) 424-8222 or (800) 662-2566, extension 3. This sequence please contact your local distributor. For technical John S. Submitted (28-JUN-1995) to the EMBL/GenBank/DDBJ databases. E-mail TECHECLONTECH.COM. NCBI gi: 988208 Stile, CLONTECH and 3" 5971..6016 /transl_table=11 /note="pid:g988212" complement (7403..8263) /note="pUC origin of replication" 6232..7403 6032..6224 5953..5970 5502..5942 /transl_table=11 /product="fusion protein" /note="pid:g988211" monoclonal antibody binding; 4768..5475 /transl_table=11 /note="pid:g988210" complement (4018..4305) 2609.. /note="pid:g988209" Location/Qualifiers /note="from ADH1 gene; contains stop codons for frame /note="encodes epitope for monoclonals Dl1 and F10 binding /note="contains Gal4 binding domain and epitopes for monoclonal antibody binding; NCBI gi: 988211" 5502..6065 /note="fl+ origin" transl_table=11/ codon_start=1/ /note="NCBI gi: 988212" /gene="ampicillin resistance" note="multiple cloning site" note="from ADH1 gene" 'gene="CYH2" codon_start= 'note="NCBI gi: 988209" 'gene="TRP1" 'note="two micron origin of replication 1..1348 organism="Cloning vector pAS2-1" note="encodes Gal4 binding domain" codon_start=1 codon_start=1 note="NCBI gi: 988210" 884..2558 2351 A; 1754 C; 1871 G; 2416 T; 1 other; Laboratories, Inc., 4030 Fabian Way, information, (B form) Palo ij 1,2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (28-JUN-1995) John S. Stile, CLONTECH Laboratories, Inc., 4030 Fabian Way, Palo Alto, CA 94303, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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May 14 13:48
                                                                                                                                CDS
                                                                                                                                                                          promoter
                                                                                 /note="contains Gal4 binding domain and epitopes for monoclonal antibody binding; NCBI gi: 988211"
                                                                                   monoclonal antibody binding;
                                                                                                                                                                          4768..5475
translation="MKLLSSIEQACDICRLKKLKCSKEKPKCAKCLKNNWECRYSPKT/
                    /product="fusion protein"
                                        transl_table=11/
                                                                 codon start=1
                                                                                                                                                    note="from ADH1
                                                                                                                                                    gene"
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36

misc_feature

5971..6016 binding"

terminator

6032..6224

note="multiple cloning site"

misc_feature misc_feature

5953..5970 5502..5942

note="encodes Gal4 binding domain"

note="encodes epitope for monoclonals D11 and F10"

EAEFPGIRRPAAKLIPGEFLMIYDFYY"

NKDAVTDRLASVETDMPLTLRQHRISATSSSEESSNKGQRQLTVSPELQYPALTHMAM KRSPLTRAHLTEVESRLERLEQLF LLIFPREDLDMILKMDSLQDIKALLTGLFVQDNV

rep_origin

and 3*

/note="from ADH1 gene; contains stop codons for frame

1,2

6232..7403

complement (7403..8263)

/note="pUC origin of replication"

/note="NCBI gi: 988212"

/gene="ampicillin resistance"

DRWEPELNEA I PNDERDTTMP VAMATT LRKLLTGELLT LASRQQ L I DWMEADKVAGP I YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRL /codon_start=1 /transl_table=11 /translation="MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY

[ELDLNSGK]LESFRPEERFPMMSTFKVLLCGAVLSR]DAGQEQLGRR]HYSQNDLVE

MEDLINE REFERENCE 유 RESULT ORIGIN REFERENCE SOURCE KEYWORDS POCUS ACCESSION DEFINITION BASE COUNT TITLE Query Match 100.0%; Best Local Similarity 76.5%; AUTHORS ORGANISM Matches JOURNAL 965 gaagttcctatactttctagagaataggaacttc 998 34 36 gaagttcctatacNNNNNNNngaataggaacttc l Cloning vector YEp213. Cloning vector YEp213 U03499 Stillman, D.J. Propagation and expression of cloned genes Rose, A.B. and Broach, J.R. Artificial sequences; Cloning vector. 1 (bases 1 to 10667) Yeast episomal vector YEp213, complete sequence 90340124 Meth. Enzymol. 185, 234-279 (1990) based vectors EP213 26; 2351 a 1754 c (bases 1 to 10667) Conservative EIGASLIKHW" LRSALPAGWF IADKSGAGERGSRG I IAALGPDGKPSR I VV I YTT GSQATMDERNRQ I A 10667 bp 1871 g Score 26; DB 61; Pred. No. 4.89e-08; 0; Mismatches DNA circular 2416 t SYN Length 8393; 1 others in yeast: 2-umcircle Indels 0; Gaps 0,

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Best Local Similarity 76.5%;
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Cloning vector YEp13
plasmid.
Yeast (Saccharomyces cerevisiae) 2
                                    K01710
                                                                Yeast (S.cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                         and Molecular Biology, University of Utah Medical Center, Salt Lake
                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-NOV-1993) David J. Stillman, Dept. of Cellular, Viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Artificial sequences; Cloning vector. 1 (bases 1 to 10667)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-NOV-1993) David J. Stillman, Dept. of Cellular, Viral
                                                   region.
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                                                                                                                                                                                                                                                                                                                                                                                              City, UT 84132 USA
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2443 c 2366 g 2969 t
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2459 c 2350 g 3021 t
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Pred. No. 4.89e-08;
                                                                2 micron plasmid
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    micron plasmid DNA
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May 14 13:48 FLP rgc

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MEDLINE REFERENCE AUTHORS REFERENCE AUTHORS ငှ BASE COUNT REFERENCE SOURCE KEYWORDS ORIGIN COMMENT FEATURES COMMENT ACCESSION DEFINITION rocas RESULT BASE COUNT FEATURES REFERENCE JOURNAL MEDLINE TITLE TITLE ORGANISM Matches Query Match 84.6%; Best Local Similarity 70.6%; TITLE JOURNAL MEDLINE AUTHORS JOURNAL AUTHORS ORGANISM source source 34 gaagttcctatacNNNNNNNngaataggaacttc 1 90 gaagttcctattctctagaaagtataggaacttc 123 39 Submitted (11-NOV-1993) David J. Stillman, Dept. of Cellular, Viral and Molecular Biology, University of Utah Medical Center, Salt Lake City, UT 84132 USA Cloning vector pRS424 Multifunctional yeast high-copy-number shuttle vectors Gene 110 (1), 119-122 (1992) efficient manipulation of DNA in Saccharomyces cerevisiae Genetics 122 (1), 19-27 (1989) 003453 57 a 47 c 46 g 103 bp upstream of XbaI site. NCBI gi: 416324 Direct Submission Stillman, D.J. Hieter,P. Christianson, T.W., Sikorski, R.S., Dante, M., Shero, J.H. and A system of shuttle vectors and yeast host strains designed Sikorski, R.S. and Hieter, P. artificial sequence; cloning vectors. Cloning vector pRS424 PRS424 5616 bp DNA circular SYN 24-MAY-1995
Yeast episomal vector pRS424 with TRP1 marker, complete sequence. NCBI gi: 172188 [1] examines whether cleavage sites are specific when the DNA-associated protein is stripped away and draws the conclusion that the specificity of DNAase I is dependent on the presence of 84138647 J. Mol. Biol. 173, 1-13 (1984) plasmid DNA chromosome Fagrelius, T.J. and Livingston, D.M. Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Endomycetales; Saccharomyces cerevisiae 92184105 89276910 nucleoprotein. Location of DNAase I sensitive cleavage sites in the yeast 2 mu-m Saccharomycetaceae. 24; (bases 1 to 5616) (bases 1 to 5616) (bases 1 to 5616) (bases 1 to 200) 1513 Conservative ၺ /organism="cloning vector pRS424" 1221 c 1356 g 1526 t /organism="Saccharomyces cerevisiae" a 47 c 46 g 50 t Location/Qualifiers 1..5616 Location/Qualifiers Score 22; DB 43; Pred. No. 1.34e-04; 0; Mismatches ;; Length Indels <u>.</u> Gaps tor ç

Query Match

84.6%;

Score

22;

DB 61;

Length 5616;

39

0

В

1 gaagttcctattcNNNNNNNnnNgtataggaacttc 34

LOCUS SOURCE KEYWORDS ACCESSION RESULT DEFINITION ORGANISM 40 Cloning vector pRS426 Cloning vector pRS426. U03451 Yeast episomal vector pRS426 with URA3 marker, PRS426 5726 bp DNA circular SYN complete sequence. 24-MAY-1995

REFERENCE TITLE AUTHORS A system of shuttle vectors and yeast host strains designed for Sikorski, R.S. and Hieter, P. artificial sequence; cloning vectors.
l (bases 1 to 5726)

REFERENCE AUTHORS MEDLINE JOURNAL efficient manipulation of DNA in Saccharomyces cerevisiae Genetics 122 (1), 19-27 (1989) Christianson, T.W., Sikorski, R.S., Dante, M., Shero, J.H. and Hieter, P. 89276910 (bases 1 to 5726)

TITLE MEDLINE JOURNAL Multifunctional yeast high-copy-number shuttle vectors Gene 110 (1), 119-122 (1992) 92184105

REFERENCE AUTHORS Direct Submission Stillman, D.J. (bases 1 to 5726)

COMMENT NCBI Submitted (11-NOV-1993) David J. Stillman, Dept. of Cellular, Viral and Molecular Biology, University of Utah Medical Center, Salt Lake gi: 416322 UT 84132 USA

source 1568 a /organism="cloning vector pRS426" 1246 c 1370 g 1542 t 1..5726 FEATURES

Location/Qualifiers

ORIGIN BASE COUNT Query Match 84.6%; Best Local Similarity 70.6%; Score 22; DB 61; Length 5726;

В 5279 gaagttcctatactttctagagaataggaacttc 5312

Matches

24;

Conservative

0;

Mismatches 10;

Indels

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Gaps

0

Pred. No. 1.34e-04;

S _ gaagttcctattcNNNNNNNgtataggaacttc 34

FOCUS SOURCE KEYWORDS RESULT REFERENCE ACCESSION DEFINITION ORGANISM AUTHORS U37458 Cloning vector YRTAG300 Cloning vector YRTAG300 CVU37458 Lieberman, B. artificial sequence; cloning vectors. (bases 1 to 6624) 6624 bp DNA circular SYN 08-NOV-1995

41 Yeast CUP1 expression-multicopy (2micron) cloning vector YRTAG300 Submitted (03-OCT-1995) Benjamin Lieberman, Pharmacology, Duke University, Research Drive, P.O. 3813, Durham, NC 27710, USA University, Research Drive, NCBI gi: 1052969 Direct Submission with the hemagglutinin tag sequence, complete sequence. selection)

> May 14 13:48 FIP rge

> > 8

ORIGIN FEATURES SG CDS misc_feature source 1845 ø LGIICVPNRKRTIDPVIARKISSLVKAYKNSSGTPKYLVGVFRNQPKEDVLALVNDYG IDIVQLHGDESWQEYQEFLGLPVIKRLVFPKDCNILLSAASQKPHSFIPLFDSEAGGT GELLDWNSISDWVGRQESPESLHFMLAGGLTPENVGDALRLNGVIGVDVSGGVETNGV KDSNKIANFVKNAKK" complement (4514..5215) region fused in frame to a start codon and and two restriction sites (SstI and XhoI) " translation="MKHTKAAWSMSVINFTGSSGPLVKVCGLQSTEAAECALDSDADL/ transl_table=11/ /codon start= 3040..3098 EIGASLIKHW" DRWEPELNEA I PNDERDTTMP VAMATT LRKLLTGELLT LASRQQL I DWMEADKVAGP L I ELD LNSGK I LESFRPEERFPMNSTFKVLLCGAVLSR I DAGQEQLGRRI I YSQNDLVE YSPVTEKHLTDGMTVRE LCSAA I TNS DNTAANLLLTT I GGPKELTAF LHNMGDHVTRL 574..1434 promoter, Cyc terminator and the hemagglutinin coding /product="N-(5'-phosphoribosyl)-anthranilate /note="NCBI gi: 1052971" /gene="TRP1" note="HA TAG with start codon" LRSALPAGWF IADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA translation="MSIQHERVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY/ /product="beta-lactamase" transl_table=11/ /codon_start=. /note="NCBI gi: 1052970" /note="based on pRS424 (TRP selection); includes CUP) /organism="Saccharomyces cerevisiae" 1543 с 1397 g 1839 t (EcoRI-HATAG-SSTI-XHOI) " isomerase"

BASE COUNT

မ 밁 Matches Best Local Similarity Query Match 6070 gaagtteetattetetagaaagtataggaaette 6103 34 gaagttcctatacNNNNNNNgaataggaacttc 1 24; Conservative 84.6%; 70.6%; Score 22; DB 84; I Pred. No. 1.34e-04; 0; Mismatches 10; Mismatches 10; Length 6624; Indels 0 Gaps <u>,</u>

CV37458 U37458; standard; circular DNA; FUN;

6624 BP

Yeast CUP1 expression-multicopy (2micron) cloning vector YRTAG300 with the hemagglutinin tag sequence, complete sequence. selection) 10-NOV-1995 (Rel. 45, Created) 10-NOV-1995 (Rel. 45, Last updated, Version 1) complete sequence. selection).

Saccharomyces cerevisiae (yeast)

Eukaryota; Plantae; Thallobionta; Eumycota; Hemiascomycetes; Endomycetales; Saccharomycetaceae

Lieberman B.; 1-6624

Submitted (03-0CT-1995) to the EMBL/GenBank/DDBJ databases.

Benjamin Lieberman, Pharmacology, Duke University, Research Drive, P.O. 3813, Durham, NC 27710, USA

NCBI gi:

1052969

Location/Qualifiers

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Best Local Similarity 70.6%;
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U33753;
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                                                                                                                                                                                                    *Isolation and characterization of a mammalian gene encoding a high-affinity cAMP phosphodiesterase*; Proc. Natl. Acad. Sci. U.S.A. 86:3599-3603(1989).
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 misc_feature
                              source
                                                                                                               Submitted (10-AUG-1995) to the EMBL/GenBank/DDBJ databases.
David J. Stillman, Division of Molecular Biology and Genetics,
                                                                                                                                                                                                                                                                                                                                                           sequence.
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                                                                        NCBI gi: 988314
                                                                                      Sciences Center, Salt Lake City, UT 84132,
                                                                                                    Department of Oncological Sciences, University of Utah Heath
                                                                                                                                                            Stillman D.J.;
                                                                                                                                                                                                                                              Wigler M.;
                                                                                                                                                                                                                                                           Colicelli J., Birchmeier C., Michaeli T., O'Neill K., Riggs M.,
                                                                                                                                                                                                                                                                          MEDLINE; 89264471.
                                                                                                                                                                                                                                                                                                                    Artificial sequences; Cloning vectors.
                                                                                                                                                                                                                                                                                                                                   Cloning vector pADNS
                                                                                                                                                                                                                                                                                                                                                                            Yeast episomal cloning vector pADNS, with ADH1 promoter, complete
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12-0CT-1995 (Rel. 45, Last updated, Version 1)
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/product="N-(5'-phosphoribosyl)-anthranilate isomerase"
/note="pid:g1052971"
BP; 1845 A; 1543 C; 1397 G; 1839 T; 0 other;
 /organism="Cloning vector pADNS"
1..38
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/gene="TRP1"
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                                                          Location/Qualifiers
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/note="based on pRS424 (TRP selection); includes CUP1
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Pred. No. 1.34e-04;
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                                                                                                                                                                                                                                                                                                                                                                 Query Match 84.6%;
Best Local Similarity 70.6%;
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Best Local Similarity 70.6%;
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                                                                                                                                      AUTHORS
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A19996
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                                       source
                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Artificial sequences" Sequence 7859 BP; 2317 A; 1656 C; 1600 G; 2286 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "PROTEINS AND NUCLEIC ACIDS";
Patent number W09109125-A/4, 27-JUN-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO: 4; Synthetic plasmid pSW6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="ADH1"
Sequence 7834 BP; 2192 A; 1672 C; 1646 G; 2324 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JUL-1995 (Rel. 44, Created)
14-JUL-1995 (Rel. 44, Last updated, Version 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A19996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               terminator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unidentified
                                                                                              Patent: WO 9207874-A 33 14-MAY-1992;
                                                                                                                                                                                                                   yeast expression vector pSW6 seq ID A18079
                                                                  NCBI gi: 513171
                                                                                                           AN INTEGRINAFFINITY SEQUENCE
                                                                                                                   PHARMACEUTICALLY ACTIVE PROTEINS COMPRISING AN ACTIVE PROTEIN AND
                                                                                                                                                               unclassified
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  2345 a
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                                      1..7984
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6381..7834
/organism="Artificial sequences"
/lab host="yeast expression vector pSW6"
| 1695 c 1638 g 2306 t
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39..505
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                                                     Location/Qualifiers
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Pred. No. 1.34e-04;
                                                                                                                                                                                                                                                                                                                                                                   Score 22; DB 88;
Pred. No. 1.34e-04;
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ORIGIN

Query Match 84.6%; Score 22; DB 34; Length 7984; Best Local Similarity 70.6%; Pred. No. 1.34e-04; Matches 24; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Db 3131 gaagttcctattctctagaaagtataggaacttc 3164
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| | ||||||||||
Cp 34 gaagttcctatacNNNNNNNgaataggaacttc 1

Search completed: Tue May 14 13:58:25 1996 Job time : 534 secs.

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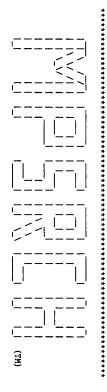
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue May 14 13:58:43 1996; MasPar time 4.93 Seconds 458.714 Million cell updates/sec

Tabular output not generated.

Title: >FLP
Description: (1-34) from frt.seq
Perfect Score: 26

N.A. Sequence: 1 gaagttcctattcNNNNNNNNytataggaacttc 34
Comp: cttcaaggataagNNNNNNNNcatatccttgaag

Scoring table: TABLE default Gap 10

Nmatch STD: Dbase 0; Query 0

thed: 84802 seqs, 33246950 bases x 2

Post-processing: Minimum Match 0% Listing first 45 summaries

n-geneseq22
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16

Statistics: Mean 5.329; Variance 3.136; scale 1.699

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. S	Score	Query Match	Query Match Length DB	BB	ID	Description	Pred. No.
c	26	100.0	54	12	067140	Complete FRT site lac	5.30e-06
2	26	100.0	1340 15	15	Q93078	Neomycin-resistance c	5.30e-06
ω	26	100.0	7859	7	Q44265		5.30e-06
4.	26	100.0	7859	~	Q12154	Shuttle vector pSW6.	5.30e-06
5	26	100.0	7984	~	Q25185	pSW6 expression vecto	5.30e-06
6	25	96.2	33	S	Q29100	Sequence of FLP recom	2.13e-05
c 7	24	92.3	41	12	Q67141	Partial FRT site lack	
∞	22	84.6	54	12	067140	Complete FRT site lac	1.28e-03
c 9	22	84.6	91	9	Q51746	Oligonucleotide probe	

2 Q12154 4 Q25185 4 Q25185 5 Q29100 12 Q671146 1 N81164 9 Q49264 9 Q49264 12 Q671367 12 Q71367 12 Q71367 12 Q71367 12 Q71366 13 Q77789 1 Q39050 1 Q39050 1 Q39050 1 Q39050 1 Q39050 2 Q10572 3 N50025 3 N50025 3 N50027 3 N5002

ALI GNMENTS

# 9	33 0 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Query Match 100.0%; Score 26; DB 12; Length 54; Best Local Similarity 76.5%; Pred. No. 5.30e-06;	LT 1 Q67140; tandard; DNA; 54 BP. Q67140; dirst entry) 22-MAR-1995 (first entry) Complete FRT site lacking additional 5 FLP binding sites. Maize; Zea mays; cereal; grass; protoplast; FLP; ss. Synthetic. M04-NIT-19-A. Q1-NIT-194; U00927. 27-JAN-1993; U5-010997. QPURDUE RES FOUND. (PURD) PURDUE RES FOUND. (PURD) PURDUE RES FOUND. Hodges TK, Lyznik LA; WPI; 94-264090/32. DNA constructs - for creating transgenic eukaryotic cells Disclosure; Page 51 79pp; English. This sequence is of the complete FRT site which is ligated into the BgIIII site of the ubiqutin first exon. This FRP site lacks additional 5 FLP protein binding sites, and has application in the construction of transgenic eukaryotic cells. Sequence 54 BP; 18 A; 9 C; 11 G; 16 T;

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34

Matches

26;

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0;

Mismatches

8

Indels

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Q93078 093078; enhancer misc_feature allograft rejection; Gal epitope; gene disruption; mouse; hyperacute rejection; xerotransplantation; Alpha-1, 3-galactosyltransferase; alpha-1, 3-GalT; transgenic animal; Neomycin-resistance cassette. misc_feature misc feature promoter Not specified. homologous recombination; knock-out; neomycin-resistance; recombination as a means of suppressing the GAL epitope. Sequence 1340 BP; 285 A; 362 C; 391 G; 302 T; The neomycin-resistance cassette given in Q93078 was used in the Disclosure; Fig.16a-16b; 184pp; English. transplants transferase gene; for eliminating hyperacute region in human New alpha-1, 3-galactosyltransferase and leukaemia inhibitor factor WPI; 95-275446/36. Robbins AJ, Crawford RJ, (BRES-) BRESATEC LTD.
(SVIN-) ST VINCENT'S HOSPITAL MELBOURNE LTD. 27-JAN-1994; US-188607. 26-JAN-1995; US-188607. WO9520661-A1. /*tag= polyA signal polyA_signal /*tag= function= herpes simplex virus /*tag= d promoter /function= polyoma virus enhancer repeats /*tag= function= FLP /*tag= function= linker sequence 10-DEC-1995 interrupt the mouse alpha-1,3-GalT gene by means of homologous development of a DNA construct (pNeo-alpha-GT10.8B) 27-JAN-1995;)3-AUG-1995. function= linker sequences function= FLP /*tag= function= herpes simplex virus /*tag= /product= corresp. DNA and nucleic acid constructs for inactivating the isc feature standard; Ф neomycin-phosphotransferase (first entry) Dapice AJF, recombinase target recombinase target site Location/Qualifiers 1..28 1250..1310 1189..1249 385..1188 250..385 105..249 29..104 cDNA; 1340 BP 1311..1340 Pearse MJ, tyrosine-kinase tyrosine-kinase site Rathjen PD; donor organ; used to

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S В 2000年間日内に S В Query Match 100.0%; Best Local Similarity 76.5%; Matches Query Match 100.0%; Best Local Similarity 76.5%; Matches LT 4 Q12154 (Q12154; LT 3 Q44265 Synthetic. W09109125-A. 3131 gaagttectattetetagaaagtataggaaette 3164 Fusion protein; blood clotting; coagulation; antithrombotic; thrombolysis; streptokinase; Sequence S. cerevisiae. used to direct export of the LD78 protein. The yeast expressivector pSW6 (NCIMB 40326) is based on the 2 micron circle from 23-DEC-1992; G02390. 23-DEC-1991; GB-027319. 14-OCT-1992; GB-021587 /*tag= circular; ds macrophage inflammatory protein; multimer; tumour therapy; psoriasis; hyperproliferation; yeast expression vector; pSW6 for expression of LD78 synthetic gene. SCI; stem cell inhibition; LD78; ACT2; MIP-lalpha; 044265 Shuttle vector pSW6. The secretion signals from the yeast mating type factor alpha were Secretion aids purification and rapid analysis of An expression vector was designed to enable secretion of LD78 Disclosure; Page 159-168; 294pp; English providing better tissue penetration alpha - unable to form stable multimer higher than dodecamer, Protein with stem cell inhibition activity, e.g. LD78 or M1P-1 WPI; 93-227322/28. Hunter MG; Craig S, (BRBI-) BRITISH BIO-TECHNOLOGY LTD. Craig S, Czaplewski LG, Edwards RM, 08-JUL-1993. W09313206-A. /note= "base illegible in the specification" misc_difference 1773 Saccharomyces cerevisiae 23-NOV-1993 (first entry) 17-SEP-1991 (first entry) the extracellular medium after expression in S. cerevisiae. 48 gaagttcctattctctagaaagtataggaacttc 81 1 gaagttcctattcNNNNNNNngtataggaacttc 34 gaagttcctattcNNNNNNNngtataggaacttc 34 standard; standard; 26; 26; 7859 BP; Conservative Conservative DNA; DNA; Location/Qualifiers 7859 7859 2317 A; 쁑 Pred. No. 5.30e-06; Pred. Score 26; Score 26; 0 0; Mismatches Mismatches 26; DB 15; No. 5.30e-06; 1667 C; DB 7; Gilbert RJ; The yeast expression fibrinolysis; plasmid; 1585 G; 00 Length 7859; .. Length 1340; LD/8 Indels circular; 2289 T; <u>.</u> <u>.</u> ç Gaps Gaps 88. 0, 0

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S 뭉 Query Match 100.0%; Best Local Similarity 76.5%; Matches Q25185; 3131 gaagttcctattctctagaaagtataggaacttc 3164 in E. vector contains an alpha factor pre-pro-peptide gene fused in frame to the gene for epidermal growth factor (EGF). The expression of (selectable marker), and an ampicillin resistant locus. The E. coli sequences are derived from E. coli ColEl-based replicon pAT153. The 07-DEC-1989; GB-027722. 07-DEC-1990; WO-G01911. 07-DEC-1990; gene encoding e.g. another hirudin protein, streptokinase or a streptokinase-like protein, via a linking peptide. This peptide this fusion is under control of a galactodse regulated promoter which contains hybrid DNA from S. cerevisiae GAL 1-10 promoter and prophylaxis. Fusion protein cleavage by blood clotting enzyme - for prodn. of fractions having greater antithrombotic activity for therapy and Dawson KM, Hunter MG, Czapleswski LG, 23-OCT-1991; G01860. 24-OCT-1990; GB-023149. ampicilin resistant locus; epidermal growth factor; GAL 1-10; Escherichia coli; 2 micron circle; shuttle vector; leu2; EGF; pSW6 expression vector. Q25185 See also Q12153-Q12156, Q12158-Q12162 and Q12490. Sequence 7859 BP; 2317 A; 1656 C; 1600 occurring are released specifically at the place where clot formation is are present at the site of the target thrombus so the active agents thrombotic activity. can be cleaved, releasing the individual proteins which have antipression vectors in which the hirudin gene is linked to a second mid was used for the expression of a synthetic hirudin HV-1 gene gene can be excised by digestion with HindIII and BamHI. The plasthe S. cerevisiae phosphoglycerate kinase (PGK) promoter. The EGF visiae and contains origins of replication for both, the leu2 gene shuttle vector capable of replcation in both E. coli and S. ceredeposited in S. cerevisiae strain BJ2168 as NCIMB 40326. The vector is based on the 2u circle from S. cerevisiae. Disclosure; Page 71; 115pp; English WPI; 91-208151/28 New proteins comprising active protein and integrin-affinity WPI; 92-183627/22. Dawson KM, Edwards RM, Fallon A; W09207874-A. phosphoglycerate kinase promoter; PGK; BamHI; HindIII; ss. (BRBI-) BRIT BIO-TECHN LTD. (BRBI-) BRITISH BIO-TECHNOLOGY LTD. 14-MAY-1992. Saccharomyces cerevisae [8-NOV-1992 (first entry) link contains a cleavage site for e.g. factor X or thrombin which 1 gaagttcctattcNNNNNNNngtataggaacttc 34 coli K12 HW87. standard; DNA; 7984 are antithrombotics useful in treating and preventing G01911. Conservative The enzymes which cleave the fusion protein The plasmid can be used to construct ex-₽₽ Pred. No. 5.30e-06; Score 26; DB 0, Mismatches 2; 1600 Length 7859; <u>...</u> Indels ç 2286 T; It is a 0; Gaps 0

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8888888888888888888888888888888 Ş 밁 Query Match Matches Best Local Similarity 76.5%; 3131 gaagttcctattctctagaaagtataggaacttc 3164 Q29100 standard; DNA; 33 Q29100; cerevisae phosphoglycerate kinase (PGK) promoter. Disclosure; Page 67; 08-MAR-1991; US-666252. 06-MAR-1992; U01899. W09215694-A. misc feature gene inactivation; ss. FLP recombinase; site-specific integration system; gene activation; Sequence of FLP recombination target site Sequence site-alpha-factor adapter-gene-BamHI site. expression vector must therefore have the general composition: HindIII the alpha-factor pro-peptide. Genes to be inserted into the pSW6 removes DNA encoding both EGF and 5 amino acids from the C-terminus of gene in pSW6 can be removed by digestion with HindIII and BamHI. terminated in this vector by the natural yeast PGK terminator. the control of an efficient galactose regulated promoter which contains hybrid DNA sequences from the S. cerevisae GAL 1-10 promoter and the S. epidermal growth factor (EGF). The expression of this fusion is under contains contains an alpha- factor pre-pro peptide fused in-frame to this greatly facilitates genetic manipulation with this vector. coli. This vector has enhanced ability for passage through amipicillin resistant locus for selection of plasmid maintenance in E. also contains the leu2 gene (a yeast selectable marker) and the coli as it contains the origin of replication for both organisms. It vector capable of replication in both S. cerevisae and Escherichia on the 2 micron circle from Saccharomyces cerevisae. The sequence given is the yeast expression vector pSW6. myocardial infarction, stroke, nucleotides in FLP recombinase is pref. 029101. The FLP recombination target site number of the 2-mu plasmid of S. cerevisiae during DNA replication. recombination reaction that is involved in amplifying the copy FLP recombinase is a protein which catalyses a site-specific Claim 33; Page 40; 49pp; English. precise modification by recombination and can be used to alter FLP-mediated gene modification in mammalian cells - giving WPI; 92-331739/40. Ogorman SV, Wahl GM; Synthetic. 25-FEB-1992 repeats, (FRT) has been identified as minimally comprising two 13 base-pair The inventors claim a mammalian recombination system in which the (SALK) SALK INST BIOLOGICAL STUDIES 17-SEP-1992. /label= spacer /*tag= ransgenes for therapeutic purposes and analysis of development. gaagttcctattcNNNNNNNngtataggaacttc 34 26; separated by an 8 base-pair spacer (see Q29100). The 7984 BP; Conservative (first entry) the Location/Qualifiers 14..21 100.0%; spacer region 2348 A; ΒP Pred. Score 26; <u>.</u> pulmonary embolism Mismatches can be replaced with any other No. 5.30e-06; 1698 C; DB 4; 1635 Length 7984; **.**. ç and deep vein Indels Transcription is It is a shuttle It is based <u>.</u>. E.coli and Gaps The 뗪 0

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RESULT
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PN W RESULT RESULT ON ACCORD OF STATE OF STA £ 맑 Ş 맑 33333g Matches Best Query Match Matches Query Match Q67140 DNA constructs - for creating transgenic eukaryotic cells Disclosure; Page 51 79pp; English. This sequence is of the complete FRT site which is ligated into the BglIII site of the ubiqutin first exon. This FRP site lacks additional 5 FLP protein binding sites, and has application in the DNA constructs - for creating transgenic eukaryotic cells Disclosure; Page 51 79pp; English. This sequence is of the partial FRT site which is ligated into the 04-AUG-1994. W09417176-A. Partial FRT site lacking additional 5 FLP binding sites. Q67141 standard; apparently missing base would be C. Sequence 33 BP; 11 A; 5 C; are separated by 8 nucleotides. NB, in the claims the sequenthe FRT has only 12 base pairs on the 3^{\prime} end of the spacer. combination of nucleotides so long as the two 13 base-pair repeats are separated by 8 nucleotides. NB, in the claims the sequence of Hodges TK, 29-JAN-1993; US-010997. 04-AUG-1994. W09417176-A. Synthetic. Maize; Zea mays; cereal; grass; protoplast; FLP; ss. Complete FRT site lacking additional 5 FLP binding sites. Q67140; construction of transgenic eukaryotic cells.
Sequence 41 BP; 13 A; 7 C; 8 G; WPI; 94-264090/32. Hodges TK, 29-JAN-1993; US-010997. 27-JAN-1994; U00927 Synthetic. Maize; Zea mays; cereal; grass; protoplast; FLP; ss. 22-MAR-1995 067141 WPI; 94-264090/32. 27-JAN-1994; U00927. 22-MAR-1995 (PURD) PURDUE RES FOUND. (PURD) PURDUE RES FOUND. Local Similarity hes 24; Conser Local 32 agttcctatactttctagagaataggaacttc 36 gaagttcctattcNNNNNNnnnnngtataggaactt 33 gaagttoctattototagaaagtataggaactt 33 agttcctatacNNNNNNNNgaataggaacttc 1 standard; site Similarity 25; of the Lyznik LA; Lyznik LA; (first entry) Conservative Conservative (first entry) DNA; DNA; 92.3**%**; 75.0**%**; 96.2**%**; ubiqutin first exon. 54 41 ВP 뫈 Score 24; DB 12; Pred. No. 8.46e-05; Score 25; DB 5; I Pred. No. 2.13e-05; 0; 0; Mismatches Mismatches 6 G; This FRP site 11 T; 13 T; œ Length Length 41; Indels Indels 33; 0 <u>.</u> Gaps Gaps ٥. <u>.</u>

Ş 8888 May 14 13:50 £ 밁 Query Match Matches Query Match Matches Best Local be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59. Sequence 91 BP; 5 A; 17 C; 15 G; 4 T; 24-MAY-1993; 108325. 26-MAY-1992; US-889651. (BECT) BECTON DICKINSON CO. Q51746; construction of transgenic eukaryotic cells. Sequence 54 BP; 18 A; 9 C; 11 G; Q93078 standard; cDNA; 1340 BP WPI; 93-378844/48. 01-DEC-1993. EP-571911-A. Synthetic. Oligonucleotide; DNA probe; mycobacteria; disease diagnosis; Oligonucleotide probe MK14-A Q51746 standard; additional 5 FLP protein binding sites, and has misc_feature allograft rejection; Gal epitope; gene disruption; mouse; hyperacute rejection; xerotransplantation; donor organ; Alpha-1,3-galactosyltransferase; alpha-1,3-GalT; transgenic animal; Neomycin-resistance cassette. Q93078; cross reacted to a few non-mycobacterial spp. Oligonucleotide probe MK14-A consists of nucleotides 5-95 of Claim 3; Page 14; 23pp; English. samples New oligo:nucleotide probes specific for Mycobacteria - used detection and amplification of Mycobacteria nucleic acid in Shank DD, 31-MAY-1994 /function= linker sequence misc_feature Not specified. homologous recombination; knock-out; neomycin-resistance; ss. 10-DEC-1995 (first entry) (Q51735). It hybridized to all spp. of mycobacteria tested, /*tag= Local <u>4</u> 19 vhvvshhhsvhhvvhhvhvsvvvvhhvvhhv 52 σ gaagttcctatactttctagagaataggaacttc gaagttcctatacNNNNNNNngaataggaacttc l gaagttcctattcNNNNNNNgtataggaacttc 84.6%; al Similarity 70.6%; 24; Conservation Similarity <u>.</u>. Spears PA; Conservative (first entry) Location/Qualifiers
1..28 cDNA; 84.6%; 91 Score 22; DB 9; Le Pred. No. 1.28e-03; 24; Mismatches 10; Score 22; DB 12; Pred. No. 1.28e-03; 0; Mismatches 9 C; FLP.mg သူ 10; <u>;</u> Length 91; 16 Length 54; The probe may application Indels 7 Indels <u>,</u> 0 ä for Gaps Gaps the 0 9

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function=

FLP

recombinase target site

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RESULT

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AC Q1

AC Q1

DT 17

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KW Fu

KW Fu

KW An

OS Sy

PN WO

PD 27

PF 07

PR 07

PR 07 ဌ 밁 Matches Query Match Best Local Similarity 70.6%; 27-JUN-1991. 07-DEC-1990; G01911. 07-DEC-1989; GB-02772 07-DEC-1990; WO-G0191 Q12154 ; Q12154; Synthetic. Fusion protein; blood clotting; coagulation; W09109125-A. antithrombotic; thrombolysis; streptokinase; Shuttle vector pSW6. Disclosure; Fig.16a-16b; 184pp; English. transplants transferase gene; for eliminating hyperacute region in human New alpha-1,3-galactosyltransferase and leukaemia inhibitor factor corresp. DNA and nucleic acid constructs for inactivating the Robbins AJ; Crawford RJ, 27-JAN-1994; US-188607. 26-JAN-1995; US-188607. /*tag= misc_feature misc_feature polyA signal /*tag= promoter promoter recombination as a means of suppressing the GAL epitope.
Sequence 1340 BP; 285 A; 362 C; 391 G; 302 T; development of a DNA construct (pNeo-alpha-GT10.8B) used to WPI; 95-275446/36. 03-AUG-1995. 17-SEP-1991 (first entry) interrupt the mouse alpha-1,3-GalT gene by means of homologous The neomycin-resistance cassette given in Q93078 was used in the (SVIN-) ST VINCENT'S HOSPITAL MELBOURNE (BRES-) BRESATEC LTD. 27-JAN-1995; IB0088 109520661-A1. function= linker sequences function= FLP *tag= function= herpes simplex virus tyrosine-kinase/ polyA_signal product= /*tag= e /function= herpes simplex virus tyrosine-kinase /*tag= d function= /*tag= 34 48 gaagttcctattctctagaaagtataggaacttc 81 gaagttcctatacNNNNNNNngaataggaacttc l standard; a neomycin-phosphotransferase polyoma virus enhancer repeats
250..385 GB-027722. WO-G01911. Conservative Dapice AJF, recombinase target DNA; 1311..1340 1250..1310 1189..1249 385..1188 84.6%; 7859 BP Pearse MJ, Rathjen PD; Pred. No. 1.28e-03; Score 22; 0; Mismatches site DB 15; LTD. plasmid; circular; ss. fibrinolysis; 10; Length 1340; Indels 0 Gaps 0

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િક 뭉 Matches Query Match 84.6%; Best Local Similarity 70.6%; 3131 gaagttcctattctctagaaagtataggaacttc 3164 Q44265 vector contains an alpha factor pre-pro-peptide gene fused in frame to the gene for epidermal growth factor (EGF). The expression of this fusion is under control of a galactodse regulated promoter which contains hybrid DNA from S. cerevisiae GAL 1-10 promoter and 23-DEC-1992; G02390. 23-DEC-1991; GB-027319. 14-OCT-1992; GB-021587. W09313206-A. circular; ds. macrophage inflammatory protein; multimer; tumour therapy; psoriasis; hyperproliferation; yeast expression vector; pSW6 for expression of LD78 synthetic gene. SCI; stem cell inhibition; LD78; ACT2; MIP-lalpha; 23-NOV-1993 (first entry) Q44265; Sequence See also Q12153-Q12156, Q12158-Q12162 and Q12490. Sequence 7859 BP; 2317 A; 1656 C; 1600 occurring. are released specifically at the place where clot formation are present at the site of the target thrombus so the active agents can be cleaved, releasing the individual proteins which have antigene encoding e.g. another hirudin protein, streptokinase or a pression vectors in which the hirudin gene is linked to a second in E. coli K12 HW87. mid was used for the expression of a synthetic hirudin HV-1 gene gene can be excised by digestion with HindIII and BamHI. The plassequences are derived from E. coli ColE1-based replicon pAT153. The visiae and contains origins of replication for both, the leu2 gene shuttle vector capable of replcation in both E. coli and deposited in S. cerevisiae strain BJ2168 as NCIMB 40326. fractions having greater antithrombotic activity for therapy and prophylaxis. Craig S, (BRBI-) BRITISH BIO-TECHNOLOGY LTD. 08-JUL-1993. /*tag= a
/note= "base illegible in the specification" misc_difference Saccharomyces cerevisiae thrombotic activity. streptokinase-like protein, via a linking peptide. This peptide the S. cerevisiae phosphoglycerate kinase (PGK) promoter. The EGF The vector is based on the 2u circle from S. cerevisiae. Disclosure; Page 71; 115pp; English. WPI; 91-208151/28 Dawson KM, link contains a cleavage site for e.g. factor X or thrombin which (selectable marker), and an ampicillin resistant locus. The E. coli 34 gaagttcctatacNNNNNNNngaataggaacttc 1 ig G standard; DNA; 7859 BP BRIT BIO-TECHN LTD. Czaplewski LG, Hunter MG, Conservative 1773 Location/Qualifiers The enzymes which cleave the fusion protein Czapleswski The plasmid can be used to construct ex-Edwards RM, Pred. No. 1.28e-03; Score 22; <u>,</u> Mismatches ទ DB Gilbert RJ; 2; 10; 1600 Length 7859; Indels င္ 2286 T; S. cere-It is a <u>,</u> Gaps 9

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PRESULT PRESUL ဌ В Query Match 84.6%; Best Local Similarity 70.6%; Matches Q25185; LT 13 Q25185 3131 gaagttcctattctctagaaagtataggaacttc 3164 this greatly facilitates genetic manipulation with this vector. pSW6 contains contains an alpha-factor pre-pro peptide fused in-frame to amipicillin resistant locus for selection of plasmid maintenance in E. coli. This vector has enhanced ability for passage through E.coli and sequence - are antithrombotics useful in treating and preventing myocardial infarction, stroke, pulmonary embolism and deep vein providing better tissue penetration Disclosure; Page 159-168; 294pp; English. Protein with stem cell inhibition activity, e.g. LD78 or MLP-1 alpha — unable to form stable multimer higher than dodecamer, WPI; 93-227322/28. expression vector must therefore have the general composition: HindIII site-alpha-factor adapter-gene-BamHI site. gene in pSW6 can be removed by digestion with HindIII and BamHI. This removes DNA encoding both EGF and 5 amino acids from the C-terminus of the control of an efficient galactose regulated promoter which contains hybrid DNA sequences from the S. cerevisae GAL 1-10 promoter and the S. epidermal growth factor (EGF). The expression of this fusion is under also contains the leu2 gene (a yeast selectable marker) and the coli as it contains the origin of replication for both organisms. It vector capable of replication in both S. cerevisae and on the 2 micron circle from Saccharomyces cerevisae. Disclosure; Page 67; 101pp; English. New proteins comprising active protein and integrin-affinity Dawson KM, Edwards RM, Fallon A; 23-OCT-1991; G01860. 24-OCT-1990; GB-023149. ampicilin resistant locus; epidermal growth factor; GAL 1-10; Escherichia coli; 2 micron circle; shuttle vector; leu2; EGF; pSW6 expression vector. Sequence vector pSW6 (NCIMB 40326) is based on the 2 micron circle from used to direct export of the LD78 protein. The secretion signals from the yeast mating type factor alpha were Secretion aids purification and rapid analysis of the extracellular medium after expression in S. cerevisiae. An expression vector was designed to enable secretion of LD78 to cerevisae phosphoglycerate kinase (PGK) promoter. The sequence given is the yeast expression vector pSW6. WPI; 92-183627/22. WO9207874-A. Saccharomyces cerevisae phosphoglycerate kinase promoter; PGK; BamHI; HindIII; ss. the alpha-factor pro-peptide. Genes to be inserted into the pSW6 terminated in this vector by the natural yeast PGK terminator. thrombosis (BRBI-) BRITISH BIO-TECHNOLOGY LTD 14-MAY-1992. 18-NOV-1992 34 gaagttcctatacNNNNNNNgaataggaacttc 1 cerevisiae. standard; 7859 BP; Conservative (first entry) DNA; 2317 A; 뙁 Pred. No. 1.28e-03; Score 22; **;** Mismatches 1698 1667 C; ç DB 7: The yeast expression 10; 1585 1635 G; Length 7859; **G**; Indels LD78. Transcription It is a shuttle Escherichia It is based 0: Gaps The EGF <u>.</u>

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င္ပ ₽ Matches Query Match Best Local Similarity /*tag= a /label= spacer (SALK) SALK INST BIOLOGICAL STUDIES Ogorman SV, Wahl GM; WPI; 92-331739/40. Q29100; 3131 gaagttcctattctctagaaagtataggaacttc 3164 FLP-mediated gene modification in mammalian cells - givir precise modification by recombination and can be used to 08-MAR-1991; US-666252 06-MAR-1992; U01899 gene inactivation; ss. Sequence of FLP recombination target site FLP recombinase; site-specific integration system; Q29100 standard; FIP recombinase is a protein which catalyses a site-specific Claim 33; Page 40; 49pp; English. transgenes for therapeutic purposes and analysis of development W09215694-A. misc feature Synthetic. 25-FEB-1992 17-SEP-1992. 34 gaagttcctatacNNNNNNNngaataggaacttc 1 24; Conservative (first entry) Location/Qualifiers 14..21 DNA; 84.6%; 70.6%; 33 ΒP Pred. Score ٥, Mismatches No. 1.28e-03 DB 4; 10; Indels Length 7984; gene activation; alter <u>,</u> Gaps 0

ဌ 밁 Query Match Best Local Similarity Matches the FRT has only 12 base pairs on the 3' end of the spacer. apparently missing base would be C. Sequence 33 BP; 11 A; 5 C; 6 G; 11 T; <u>ي</u> 1 gaagttcctattctctagaaagtataggaactt 33 gaagttcctatacNNNNNNNNgaataggaactt 23; Conservative 80.8%; 69.7%; Score 21; DB 5; I Pred. No. 4.88e-03; ç Mismatches 10; Length 33; Indels **.**: Gaps ç

are separated by 8 nucleotides. NB, in the claims the sequence combination of nucleotides so long as the two 13 base-pair repeats nucleotides in the spacer region can be replaced with any other FLP recombinase is pref. Q29101. The FLP recombination target site number of the 2-mu plasmid of S. cerevisiae during DNA replication. recombination reaction that is involved in amplifying the copy

(FRT) has been identified as minimally comprising two 13 base-pair The inventors claim a mammalian recombination system in which the

separated by an 8 base-pair spacer (see Q29100). The

RESULT RSAEBARB Q67141; Partial FRT site lacking additional 5 FLP binding sites Maize; Zea mays; cereal; grass; protoplast; FLP; ss. Synthetic. 22-MAR-1995 (first entry) Q67141 standard; H09417176-A DNA; 41 ВP

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RESULT
ID NE
AC NE
DT 08
DE Ba
KW E. S 닭 S 밁 Query Match Best Local S Best Local Similarity Matches 22; Conser Matches Query Match JLT 16 Q51746 standard; Q51746; This sequence is or the ubiquith first exon. This FKF site is additional 5 FLP protein binding sites, and has application in the construction of transgenic eukaryotic cells.

13 A; 7 C; 8 G; 13 T; LT 17
N81164 standard; DNA; 204 BP.
N81164;
N8-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase alpha-fragment. DNA conservation --Disclosure; Page 51 79pp; English.

This sequence is of the partial FRT site which is ligated into the This sequence is of the partial FRT site which is ligated into the results of the partial FRT site which is ligated into the be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59. Sequence 91 BP; 5 A; 17 C; 15 G; 4 T; Oligonucleotide probe MK14-A
Oligonucleotide; DNA probe; mycobacteria; disease diagnosis; cross reacted to a few non-mycobacterial spp. Oligonucleotide probe MK14-A consists of nucleotides 5-95 of Claim 3; Page 14; 23pp; English. WPI; 93-378844/48. Shank DD, 26-MAY-1992; US-889651 24-MAY-1993; 108325 01-DEC-1993. EP-571911-A. Synthetic. 31-MAY-1994 DNA constructs - for creating transgenic eukaryotic cells WPI; 94-264090/32. (PURD) PURDUE RES FOUND. Hodges TK, Lyznik LA; 27-JAN-1994; U00927. 29-JAN-1993; US-010997. 04-AUG-1994. 8amp⊥es detection and amplification of Mycobacteria nucleic acid (Q51735). It hybridized to all spp. of mycobacteria tested, New oligo:nucleotide probes specific for Mycobacteria - used (BECT) BECTON DICKINSON CO 12 svhsyyvvhvvshhhsvhhvvhhvhvsvvvvhhv 45 1 gaagttcctattcNNNNNNngtataggaacttc 34 ω 5 agtteetataetttetagagaataggaaette 36 agttcctattcNNNNNNNngtataggaacttc 34 beta galactosidase alpha-fragment; Similarity 0 Spears PA; Conservative Conservative (first entry) cDNA; 91 BP 76.9%; 68.8%; 76.9%; Pred. No. 1.83e-02; 23; Mismatches 11 Score 20; Score 20; DB 12; Pred. No. 1.83e-02; <u>.</u>. Mismatches **B**G base substitutions; 9; 10; Length 91; Length 41, The probe may Indels Indels 'n 0 0; but tor Gaps Gaps 0 9

RESULT
AC Q44
AC Q44
AC Q44
AC C6
AC C6
KW L6
KW AL
KW မှ 밁 May 14 13:50 Matches Query Match 61.5%; Best Local Similarity 18.5%; Q49264; 28-APR-1994 exon exon exon exon Q49264 Introducing random point mutations into nucleic acods -by prepn of single stranded template, annealing a primer, misincorporation, completion of molecules and screening. occurred singularly in any given mutant. See also P80575. transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which /*tag= primer_bind /*tag= /*tag= /*tag= /*tag= Caenorhabditis briggsae. mammal; probe; ds. Alzheimer's disease; cell death gene; PCR; polymerase chain reaction; ciona intestinalis; echinoderm; lamprey; puffer fish; hybridisation; lower organism; structural homologue; ced-4. Sequence variable 3' ends generated in this way are used as primers for possible nucleotide positions within a specified region. The it to generate a popn of DNA molecules which terminate at all single stranded template and an oligonucleotide was hybridised E.coli beta-galactosidase. The wild type sequence was obtained Disclosure; p; English. Lehtovaara P, Knowles J, Koivula A, Bamford J, Reinikainen WPI; 88-279927/40. 03-APR-1987; US-034819. 05-MAY-1988. EP-285123-A. misc_feature Escherichia coli. /*product= ced-4_ Long-distance homology; evolution; nematode; reverse transcriptase. Nucleotides are misincorporated by the Random point mutations were introduced into the alpha fragment (SUSO) SUOMEN SOKERI OY. 30-MAR-1988; 105163. /function=multiple cloning site /*tag= /*tag= 159 hvchnvhbnnhrnwayvrhdarrddvh 185 29 tcctatacNNNNNNNngaataggaact 3 standard; DNA; 4093 BP ىھ æ n 6 5; 204 BP; (first entry) Conservative 19..69 Location/Qualifiers 459..3246 gene_product 187..204 1651..1716 1383..1472 986..1081 Location/Qualifiers 21 A; Score 16; DB 1; L Pred. No. 2.91e+00; 15; Mismatches 47 C; FLP mg 17 G; 11 T; Length 204; 7; Indels 108 Others elongation, -3 0 Gaps ς as of. a 0

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RESULT LT 20 Q10572 standard; DNA; Q10572; NPRB analogues. The protein has a mol wt. of 115 kD (calculated Mr receptor B, NPRB, having guanyl cyclase (GC) activity and protein kinase activity. The DNA can be inserted into expression vectors for the prodn. of the protein, opt. after being mutated to produce N-PSDB; Q10324.
Natriuretic protein receptor B - for diagnosis and treatment of (GETH) GENENTECH INC. Chang M, Goeddel D, Lowe WPI; 91-036711/05. /label= N-glycos_site Modified -site 195..197 /label= N-glycos_site Modified -site 161..163 Human Natriuretic Peptide Receptor B.
NPRB; ANP; ENP; kidney failure; heart failure; protein kinase; also affinity chromatography. Antibodies with affinity for NPRB natriuretic peptide disorders, and also to isolate peptides using 22-JUN-1990; U03586. 23-JUN-1989; US-370673. /label= N-glycos_site Modified -site 600..602 Modified -site /label= N-glycos_site Modified -site 277..279 /label= N-glycos_site Modified -site 244..246 Modified -site Modified -site 24..26 Domain Domain Domain Protein Peptide /label= signal 09-APR-1991 (first entry) The sequence was derived from the DNA encoding natriuretic peptide Claim 3; Fig 1; 49pp; English. kidney failure, heart failure, hyperaldosteronism, 709100292-A /label= N-glycos_site Modified -site 349..351 /label= N-glycos site Modified -site 35..37 /note= "binds natriuretic peptides hyperaldosteronism; glaucoma; guanyl cyclase. /note= "GC and protien kinase /label= cytoplasmic domain /label= transmembrane domain /label= extracellular domain /label= mature NPBR tomo sapiens. 14, 952). 0-JAN-1991. label= N-glycos_site 8 prepd. 1047 The protein (or variants) can be used in treatment of sequence ₿₽; 479..1047 Location/Qualifiers 1..22 456..456 23..455 1047 87 A; Ç. ВP activity' 15 Ç A, B and 83 G; ್ಷ Length 1047; 51 glaucoma etc. ;;

Matches

Conservative

Pred. No. 9.70e+00; Score 15; 13;

DB 2;

Mismatches

Indels

<u>,</u> Gaps

0

Query Match 57.7%; Best Local Similarity 21.2%;

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RESULT
ID Q7
AC Q7
D7 21
DE E.
KW C. ÷ 뭉 မှ В Matches Query Match 57.7%; Best Local Similarity 61.3%; 071367; 21-APR-1995 (first entry) E.coli/S.cerevisiae shuttle vector pMTL8100. T 22 Q71367 standard; antagonists, or to profile other agents which are potentially therapeutic for alzheimers disease.

Sequence 1971 BP; 620 A; 440 C; 436 G; 475 T; study, diagnosis and therapy of Alzheimer's disease Claim 8; Page 49-51; 78pp; English. Kozlowski MR, Manly SP, Neve RL; WPI; 94-101215/12. /product= Beta W09405811-A. T 21 Q56791 standard; cDNA; 1971 Cassette; gene expression; promoter; recombinant protein; C100-R sequence may be utilised to block transcription and expression of the or ribozyme molecules designed on the basis of the C100-R DNA precursor protein (the C100-R) and so facilitates the elucidation of the function of C100-R and its role in the development of Alzheimers P-PSDB; R50951. 31-AUG-1992; US-938184. 31-AUG-1993; U08229. 17-MAR-1994. antagonist; antisense; ribozyme; beta amyloid precursor protein, transgenic animal; diagnosis; detection; therapy; agonist; cDNA encoding receptor for C-terminus of beta-amyloid precursor. 07-0CT-1994 (first entry) effects of the beta amyloid precursor protein-C100 agonists or DNA as the transgene may be engineered to determine the in vivo diagnostic imaging in vivo. determine the pattern of receptor expression in biopsy tissue, or for autopsies to diagnose abnormalities of C100-R expression. disease. The cDNA encodes a receptor for the C-terminus of the beta amyloid Cloning and expression of beta APP-C100 receptor - facilitating (MCLE-) MCLEAN HOSPITAL CORP. (BRIM) BRISTOL-MYERS SQUIBB CO. 30-AUG-1993; US-938184. /*tag= Rattus rattus. C100-R; ss. Receptor; precursor protein; alzheimers disease; antibodies; Q56791; 31 gttcctatacNNNNNNNngaataggaacttc 1 జ్ఞ 83 gaagttcctatacNNNNNNNngaataggaactt 2 savdnknyhdndnnngngcvynaasvarnashw 115 :- :: gene. മ 19; It may be used in hybridisation assays of biopsies or Conservative Antibodies specific for the C100-R may be used to amyloid precursor protein receptor. DNA; Location/Qualifiers 3249 쁑 Pred. No. 9.70e+00; ₽P = :::: Score 15; <u>.</u> Transgenic animals containing the C100-R Mismatches DB 10; 12; Length 1971; Indels <u>.</u>. Antisense Gaps 9

Best Query Match Matches constructed by isolating a 1.4kb Rsal fragment which encompassed origin of replication and STB locus of the 2mm plasmid, from plass pVT100-U and inserting it into the unique EcoRV site of pMTLCJ. Plasmid pMTLCJ was constructed essentially by cloning a 0.8 kb BamHI fragment encoding chloramphenicol acetyltransferase (cat) f plasmid pCM4 (Close and Rodriguez, 1982) into the BamHI site of /*tag= Q71366 standard; DNA; 3400 the modified cat gene excised as a 0.8 kb BamHI fragment, which was This shuttle vector has the replicative functions of an E.coli plasmid as well as those of a S.cerevisiae plasmid. The vecto /product= Chloramphenicol acetyltransferase W09419472-A. misc_signal Synthetic. 2 mu plasmid; Cassette; gene expression; promoter; recombinant protein; E.coli/S.cerevisiae shuttle vector pMTL8000. 21-APR-1995 (first entry) Q71366; Sequence al., 1988), encompassing the replication region of plasmid pMTL4 (Chambers et then blunt ended and ligated to a 1.1kb SspI/DraI fragment stranded DNA of the mutated M13 recombinant was then prepared and to eliminate restriction sites from the cat structural gene. Double was then used as a template in successive site directed mutagenesis M13mp8. Example 3; Page 32-34; 48pp; English protein expression in bacteria and yeast esp modified yeast promoter, provides high level of recombinant New promoter DNA with unique SspI site at gene start position -WPI; 94-294335/36. Faulkner JDB, 25-FEB-1994; G00373. 01-SEP-1994. misc_teature misc_signal Synthetic. fermentation; 116 ataggaacttcggaataggaacttc 140 (PUBL-) PUBLIC HEALTH LAB SERVICE 26-FEB-1993; GB-003988. /*tag= /label= STB /*tag= /label= 2mu replication region fermentation; y Match 57.7%; Local Similarity 64.0%; 25 mu plasmid; atacNNNNNNNgaataggaacttc 16; Single stranded DNA prepared from the resulting recombinant 3249 BP; to give pMTLCJ. Locus. Conservative Minton NP; g. ė heterologous heterologous gene; clone; cloning; yeast; bacteria; Location/Qualifiers 3154..3376 2375..2666 Location/Qualifiers 3003..3225 61..1117 882 A; 뮱 gene; Score 15; DB 12; Pred. No. 9.70e+00; 0, clone; cloning; yeast; Mismatches 693 C; BOARD. DB 12; Length 3249; 743 9; ç; Indels 931 The vector was bacteria; from plasmid 0 Gaps from the 0

TTTESE SEE E DA CI

/label= 2mu

replication region

운 문

misc_feature

2526..2817

j

မှ В Matches Query Match 57.7%; Best Local Similarity 64.0%; Q77789 standard; DNA; 5211 BP /codon= seq:CAA, aa:Lys w09423024-A. /*tag= eliminating the SspI restriction site using the plasmid site pVT100-U and inserting it into the unique EcoRV site of pMTLJ. Plasmid pMTLJ was derived from pMTLA (Chambers at al., 1988), by origin of replication and STB locus of the 2mu plasmid, plasmid as well as those of a S.cerevisiae plasmid. The vector was constructed by isolating a $1.4 \rm kb$ RsaI fragment which encompassed the New promoter DNA with unique SspI site at gene start position - esp modified yeast promoter, provides high level of recombinant protein expression in bacteria and yeast Example 3; Page 30-32; 48pp; English. 07-APR-1994; U03441. 07-APR-1993; US-043747. misc_difference 480..482 sig_peptide G+C content; Pre-pro-cobra C3 coding sequence. Q77789; directed mutagenesis method. This shuttle vector has the replicative functions of an E.coli WPI; 94-294335/36. 01-SEP-1994. WO9419472-A. misc_difference 483..485 /codon= seq:GAA, aa:Asp mat_peptide /product= Pre-Naja naja X. laevis; pre-pro molecule; beta chain; alpha chain; codon usage; Cobra; C3; third component of complement; human; mouse; rat; 26-JUN-1995 (first entry) Faulkner JDB, (PUBL-) PUBLIC HEALTH LAB SERVICE BOARD 26-FEB-1993; GB-003988. 25-FEB-1994; G00373 /product= Beta /*tag= c /label= STB locus /*tag= /tag= /*tag= b 116 ataggaacttcggaataggaacttc 140 8 13-0CT-1994. /*tag= *tag= 25 atacMNNNNNNngaataggaacttc 1 Ω o ø AIND 16; 3400 BP; immune response; host defence; ss. Conservative GEORGETOWN Minton NP; .pro-cobra C3 lactamase 9..74 Location/Qualifiers 9..4964 75..4961 444..1304 917 A; Pred. No. Score 15; 0; Mismatches 738 C; DB 12; 1 9.70e+00; 787 G; 9. Length 3400; Indels 958 T; from plasmid 0; Gaps 0

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မှ 밁 Query Match 57.7%; Best Local Similarity 60.6%; Matches chain comprises 992 amino acids and the beta chain comprises 633 residues, being 12 residues shorter than the human beta chain. Col C3 has a different codon usage compared to mammalian C3 mRNAs. The C+C content of all known mammalian C3 mRNAs is more than 53%. The 31-AUG-1992; 114838. 04-SEP-1991; IT-MI2349. Genetic; vector; integration; Kluyeromyces lactis; 255 ribosomal DNA; Saccharomyces cerevisiae; E. coli; domain; yeast; plasmid; promoter; expression cassette; HIS3; marker; transformant; human; lysozyme; HIZ; Q39050; Q39050 standard; G+C content of cobra C3 mRNA is significantly lower at 43%. The significance of this difference is not known. C3 is thought to have into the mature two-chain protein by removing the signal peptide and the four Arg residues between the beta and alpha chain. The alpha molecules from human, mouse, rat and X. laevis. Cobra C3 is Claim 1; Fig 2A-2L; 155pp; English. Bredehorst event has occured. Galeotti CL, Galle WPI; 93-127394/16. K.lactis/S. cerevisae genetic vector. Sequence synthesised as a pre-pro molecule that is subsequently processed The cDNA sequence of cobra C3 shows a high sequence homology with treatment of cancer DNA encoding cobra C3, P-PSDB; R63222 WPI; 94-333186/41. integrating unit consisting of two not contiguous sequences of the 2 ribosomal DNA from S. cerevisiae, flanking a genetic marker suitable maintenance of the plasmid in E. coli and a domain which acts as an integrating vector which comprises a region necessary for the stable multiple integration of DNA sequences into the genome of Kluyeromyces This sequence represents a genetic vector which allows the stable Claim 1; Fig 1; 26pp; English. heterologous proteins which allows stable multiple integration of DNA for prodn. of Vector for Kluyeromyces lactis and Saccharomyces cerevisiae (ISTS) SCLAVO SPA. 21-APR-1993. EP-537456-A. Synthetic FLP; 2 micron plasmid; ss. GALT; signal sequence; killer toxin; transcription termination signal; 28-JUL-1993 (first entry) This sequence encodes the cobra C3 (third component of complement). for the from K. lactis and S. cerevisiae is pref. used as a genetic marker integration plasmid, such as expression cassettes. for selection of the yeast transformants in which the integration lactis and Saccharomyces cerevisiae. This sequence can be used in an 711 aagtttctttacattgatgggaataaaaatttc 743 important functions in the immune response and host defence. 33 aagttcctatacNNNNNNNngaataggaacttc 1 selection of transformants and an expression 20; 5211 BP; Conservative Gallo E, Fritzinger DNA; 6824 Other DNA sequences may be introduced into the Riccio 1612 A; CVF 1 and CVF 2 - which are Ď, ΒP Score 15; DB 13; Pred. No. 9.70e+00; 0; ŗ, Vogel C; Mismatches 1042 C; Rossolini GM, 13; 1201 G; Length 5211; Indels Thaller MC; used The gene HIS3 cassette for the in the 1356 T; <u>,</u> of the 255 Gaps ឩ 0

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RESULT
RE 88888888 S 맑 밁 Best Query Match Matches Matches Best Local Similarity 18.5%; Query Match LT 26 N81164 integration vector of the invention and an expression cassette comprising the K. lactis GAL7 promoter, the signal sequence of the K. lactis killer toxin, the cDNA encoding the ripe form of human lysozyme 2506 gaagttcctattccgaagttcctat 2530 E.coli beta galactosidase alpha-fragment; base substitutions; ss. Base substituted E.coli beta-galactosidase alpha-fragment. Sequence production and secretion into the culture medium Sequence See also P80575. occurred singularly amplified and then expressed in a suitable host-vector system. The sequence covers all 176 difft base substitutions, most of which amplified and then expressed in a suitable host-vector system. reverse transcriptase. Nucleotides are misincorporated by the possible nucleotide positions within a specified region. The it to generate a popn of DNA molecules which terminate at all single stranded template and an oligonucleotide was hybridised to E.coli beta-galactosidase. The wild type sequence was obtained Random point mutations were introduced into the alpha fragment Disclosure; p; English misincorporation, completion of molecules and screening. by prepn of single stranded template, annealing a primer, elongation, WPI; 88-279927/40. (SUSO) SUOMEN SOKERI OY. Lehtovaara P, Knowles J, Koivula A, 03-APR-1987; 30-MAR-1988; 05-MAY-1988. EP-285123-A. primer_bind misc feature Escherichia coli 08-NOV-1990 (first entry) N81164; plasmid from S. (HLZ) and the transcription termination signal FLP of the 2 micron This complete transformation vector is 7850 bp long and includes variable 3' ends generated in this way are used as primers for /*tag= function=multiple cloning site /*tag= a introducing random point mutations into nucleic acods -159 hvchnvhbnnhrnwayvrhdarrddvh 185 y Match 57.7%; Local Similarity 64.0%; 1 gaagttcctattcNNNNNNNngtat 25 standard; DNA; 16; Š 6824 204 BP; US-034819. Conservative 105163 Conservative ₽₽; cerevisiae. 19..69 187..204 Location/Qualifiers 53.8%; in any given mutant. 21 A; 204 BP 1815 A; Pred. No. 9.70e+00; Score 15; DB 7; 14; Pred. No. 3.13e+01, Score 14; <u>.</u> 47 C; Mismatches Mismatches 1521 C; 17 G; Bamford J, DB 1; 11 T; 1726 G; Length 6824; œ 9 Length 204; Reinikainen of. Indels Indels human lysozyme. 108 Others; 1762 T; 0. <u>.</u>. Gaps as e, Gaps the Ω <u>,</u> 0

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6 tcctattcNNNNNNNgtataggaact 32

ဌ В Query Match 53.8%; Best Local Similarity 42.4%; Matches /*tag= a EP-163993—A. N50034; N50034 Sequence encoding new modified human beta interferon polypeptides IFNX 418. (SEAR) SEARLE G D & CO. Bell LD, Boseley PG, Por WPI; 85-311944/50. New modified human beta interferon polypeptide(s) - pplasmid transformed bacteria, with improved antiviral (SEAR) SEARLE G D & CO. Bell LD, Boseley PG, Por WPI; 85-311944/50. 04-SEP-1991 N50025 standard; DNA; 501 Sequence breakdown during synthesis; and better in vivo solubility and stability. They are also easier to recover from incubation mi have higher therapeutic index; improved stability against microbial New modified human beta interferon polypeptide(s) - pr plasmid transformed bacteria, with improved antiviral, /*tag= 04-SEP-1991 P-PSDB; P50024. Homo sapiens antiproliferative; ss. Antiviral; cell growth regulator; N50025; Compared with interferon beta prepd. by recombinant methods, the Claim 28; Chart 21, page 43; 71pp; English. anti-proliferative and immune regulating actions P-PSDB; P50033. 17-MAY-1984; GB-012564 17-MAY-1985; EP-163993-A. Homo sapiens. antiproliferative; ss. Antiviral; cell growth regulator; Sequence encoding new modified human beta interferon polypeptides 17-MAY-1984; GB-012564 17-MAY-1985; 105750. 116 arathccnatggaratgacngaraargarttyc 148 for cell surface receptors (allowing selective targetting); they INFs of the invention are more active and have different affinities l1-DEC-1985. 11-DEC-1985. FNX 485. 33 aagttcctatacNNNNNNNgaataggaacttc 1 27 standard; DNA; 498 14; 498 BP; Conservative (first entry) (first entry) Location/Qualifiers Location/Qualifiers Porter Porter 112 A; ВP ₽₽ AG; Pred. No. 3.13e+01; AG; Score 14; 6; Mismatches 30 C; immune immune system regulator; DB 3; system regulator; 83 from incubation G; 77 T; 13; Length 498; Indels prepd. prepd. by ý <u>.</u> mixts Gaps 0

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DT 04 밁 S В Ş Query Match Query Match 53.8%; Best Local Similarity 22.6%; Matches Query Match 53.8%; Best Local Similarity 22.6%; Matches N50026; 04-SEP-1991 (first entry) have higher therapeutic index; improved stability against mice breakdown during synthesis; and better in vivo solubility and stability. They are also easier to recover from incubation mi Sequence 501 BP; 107 A; 31 C; 69 G; 80 T; N50023; N50023 standard; Claim 28; Chart 2c, page 34; 71pp; English.

Compared with interferon beta prepd. by recombinant methods, the INFs of the invention are more active and have different affinities Antiviral; cell growth regulator; immune system regulator; Sequence encoding new modified human beta interferon polypeptides stability. N50026 standard; DNA; 501 BP Compared with interferon beta prepd. by recombinant methods, the Claim 28; Chart 2a, page 32; 71pp; English. anti-proliferative and immune regulating actions plasmid transformed bacteria, with improved antiviral, New modified human beta interferon polypeptide(s) - prepd. by WPI; 85-311944/50. Bell LD, Boseley PG, Porter AG; EP-163993-A. /*tag= Homo sapiens. antiproliterative; ss. 04-SEP-1991 (first entry) breakdown during synthesis; and better in vivo solubility and have higher therapeutic index; improved stability against microbial for cell surface receptors (allowing selective targetting); they anti-proliferative and immune regulating actions P-PSDB; P50022. for cell surface receptors (allowing selective targetting); they INFs of the invention are more active and have different affinities (SEAR) SEARLE G D & CO. 17-MAY-1984; GB-012564. 17-MAY-1985; 105750 l1-DEC-1985. IFNX 416. 15 bytbggnttyytbcarmgdwnnwnnaaytty 45 15 bytbggnttyytbcarmgdwnnwnnaaytty 45 4 gttcctattcNNNNNNngtataggaacttc 34 4 gttcctattcNNNNNNNgtataggaacttc 34 29 ೪ 7; 501 BP; They are also easier to recover from incubation mixts. 501 BP; 112 A; 30 C; 69 G; 85 T; Conservative Conservative Location/Qualifiers DNA; 501 BP. :: :: :: Pred. No. 3.13e+01 Score 14; Pred. No. Score 14; 9; 9; Mismatches 30 C; Mismatches 3.13e+01; DB 3; DB 3; 69 G; 15; 15; Length 501, Length incubation mixts 85 T; Indels Indels 501; microbial <u>.</u> <u>.</u>. Gaps Gaps 0 <u>.</u>

S 밁 May 14 13:50 Best Loc Matches Query Match plasmid transformed bacteria, with improved antiviral, anti-proliferative and immune regulating actions Claim 28; Chart 2i, page 40; 71pp; English. Compared with interferon beta prepd. by recombinant methods, the INFs of the invention are more active and have different affinities (SEAR) SEARLE G D & CO. Bell LD, Boseley PG, Por WPI; 85-311944/50. 04-SEP-1991 (first entry) N50031 standard; DNA; 501 breakdown during synthesis; and better in vivo solubility and anti-proliferative and immune regulating actions Claim 28; Chart 2d, page 35; 71pp; English. Compared with interferon beta prepd. by recombinant methods, the New modified human beta interferon polypeptide(s) - puplasmid transformed bacteria, with improved antiviral, antiproliferative; Bell LD, Boseley PG, Porter AG; WPI; 85-311944/50. 11-DEC-1985. 17-MAY-1985; 105750. EP-163993-A. Homo sapiens. antiproliferative; Antiviral; cell growth regulator; immune system regulator; Sequence encoding new modified human beta interferon polypeptides N50031; Sequence stability. have higher therapeutic index; improved stability against microbial P-PSDB; P50025. 17-MAY-1985; 105750. 17-MAY-1984; GB-012564. EP-163993-A. Homo sapiens. Antiviral; cell growth regulator; immune system regulator; Sequence encoding new modified human beta interferon polypeptides New modified human beta interferon polypeptide(s) -P-PSDB; P50030. (SEAR) SEARLE G D & CO. 17-MAY-1984; GB-012564. IFNX 448. for cell surface receptors (allowing selective targetting); they INFs of the invention are more active and have different affinities 11-DEC-1985. IFNX 430 15 bytbggnttyytbcarmgdwnnwnnaaytty 45 Local Similarity 4 gttcctattcNNNNNNNgtataggaacttc surface receptors (allowing selective targetting); they 501 BP; 53.8%; ilarity 22.6%; Conservative They are also easier to recover from incubation mixts. 501 BP; 108 A; 31 C; 70 G; 81 T; 1..501 Location/Qualifiers 1..501 Location/Qualifiers ss. 88. Porter 108 A; ВP Score 14; DB 3; Pred. No. 3.13e+01 9; 31 C; Mismatches FI.P.mg 34 ç 15; Length 501; Indels prepd. by 0 Gaps 0

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Bell LD, Boseley PG, Porter AG;
WPI; 85-311944/50. Sequence encoding new modified human beta interferon polypeptides IFNX 446. stability. antiproliferative; Antiviral; cell growth regulator; immune system regulator; Sequence encoding new modified human beta interferon polypeptides Sequence stability. breakdown during synthesis; and better in vivo solubility and Claim 28; Chart 2g, page 38; 71pp; English.

Compared with interferon beta prepd. by recombinant methods, the anti-proliferative and immune regulating actions plasmid transformed bacteria, with improved antiviral, New modified human beta interferon polypeptide(s) -P-PSDB; P50028. EP-163993-A. antiproliferative; ss. Antiviral; cell growth regulator; immune system regulator; 04-SEP-1991 (first entry) N50029; Sequence have higher therapeutic index; improved stability against microbial 11-DEC-1985. 17-MAY-1985; 105750. Homo sapiens. IFNX 444. for cell surface receptors (allowing selective targetting); they INFs of the invention are more active and have different affinities 17-MAY-1984; GB-012564. 15 bytbggnttyytbcarmgdwnnwnnaaytty 45
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:::|: ||: 15 bytbggnttyytbcarmgdwnnwnnaaytty 45 4 gttcctattcNNNNNNngtataggaacttc 34 4 gttcctattcNNNNNNNngtataggaacttc 34 501 501 BP; They are also easier to recover from incubation mixts 501 BP; 112 A; 31 C; 69 G; 79 T; They are also easier to recover from 501 BP; 110 A; 30 C; 69 G; Conservative Conservative (first entry) DNA; Location/Qualifiers DNA; 53.8%; 501 BP 501 BP :: :: :: .. =:=: Score 14; DB 3; Pred. No. 3.13e+01 Pred. No. 3.13e+01 Score 14; 9 9; Mismatches Mismatches DB 3; Length 501; Length 501; 15; 15; incubation mixts. 80 T; Indels Indels prepd. and microbial <u>..</u> 0 Gaps Gaps 0 0

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Best Local Similarity 22.6%;
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EP-163993-A.
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                                                                               anti-proliferative and immune regulating actions Claim 28; Chart 2j, page 41; 71pp; English. Compared with interferon beta prepd. by recombinant methods, the INFs of the invention are more active and have different affinities
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plasmid transformed bacteria, with improved antiviral,
breakdown during synthesis; and better in vivo solubility and stability. They are also easier to recover from incubation mixts. Sequence 501 BP; 108 A; 30 C; 72 G; 79 T;
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plasmid transformed bacteria, with improved antiviral,
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                                               for cell surface receptors (allowing selective targetting); they have higher therapeutic index; improved stability against microbial
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                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                antiproliferative; ss.
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Pred. No. 3.13e+01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                 immune system regulator;
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Query Match

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Length 501;

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KW ₽ δ S 문 Matches Query Match 53.8%; Best Local Similarity 22.6%; Matches EP-163993-A. 11-DEC-1985. Sequence encoding new modified human beta interferon polypeptides .T 36 N50033 standard; Sequence encoding new modified human beta interferon polypeptides IFNX 417. Homo sapiens. antiproliferative; ss. Antiviral; cell growth regulator; immune system regulator; 04-SEP-1991 N50033; stability. breakdown during synthesis; and better in vivo solubility and have higher therapeutic index; improved stability against microbial Claim 28; Chart 2b, page 33; 71pp; English. Compared with interferon beta prepd. by recombinant methods, the anti-proliferative and immune regulating actions plasmid transformed bacteria, with improved antiviral, New modified human beta interferon polypeptide(s) -P-PSDB; P50023. Bell LD, Boseley PG, Porter AG; EP-163993-A. Homo sapiens. antiproliferative; Antiviral; cell growth regulator; immune system regulator; 04-SEP-1991 (first entry) N50024 N50024 IFNX 456. WPI; 85-311944/50. /*tag= for cell surface receptors (allowing selective targetting); they INFs of the invention are more active and have different affinities (SEAR) SEARLE G D & CO. 17-MAY-1984; GB-012564 17-MAY-1985; 105750. 11-DEC-1985. /*tag= 15 bytbggnttyytbcarmgdwnnwnnaaytty 45 15 bytbggnttyytbcarmgdwnnwnnaaytty 45 ::1: ||: :: : ||:||: 4 gttcctattcNNNNNNNgtataggaacttc 34 4 gttcctattcNNNNNNNngtataggaacttc 35 standard; DNA; 501 BP a 501 BP; Conservative They are also easier to recover from incubation mixts Conservative (first entry) Location/Qualifiers DNA; Location/Qualifiers 88. 501 BP 110 A; Score 14; DB 3; L Pred. No. 3.13e+01; 9; Mismatches 9; 32 C; Mismatches ω 66 G; 15; 15; Length 501; 81 Indels Indels prepd. ... by 0 <u>,</u> Gaps Gaps ç 0

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₽ 밁 RESULT yuery Match 53.8%; Score 14; Best Local Similarity 22.6%; Pred. No. Matches Query Match 53.8%; Best Local Similarity 59.4%; Matches 1327 aaatttcttttctatgaataatagaggaactt 1358 rat cDNA clone RL-39(10) as probe. One clone (I)-1 was purified, sequenced. The sequence is expected to be useful for genetic Claim 3; Fig 2; 9pp; Japanese. This sequence encodes human cysteine dioxygenase. A cDNA library was urinary diseases 01-MAY-1992. cystine; genetic diagnosis; cystine urine diseases; ss. Encodes human liver cysteine dioxygenase. Q25420 standard; DNA; 1561 BP. Q25420; have higher therapeutic index; improved stability against microbial breakdown during synthesis; and better in vivo solubility and stability. They are also easier to recover from incubation mixts. Sequence 501 BP; 111 A; 31 C; 68 G; 80 T; Claim 28; Chart 2k, page 42; 71pp; English.

Compared with interferon beta prepd. by recombinant methods, Bell LD, Boseley PG, WPI; 85-311944/50. diseases, diagnosis and treatment, esp. for the treatment of cystine urine tissue from a liver cancer patient. The library was screened with prepared using polyA+ RNA separated from human non-cancer liver Human liver cysteine di:oxygenase and cDNA used for its encoding P-PSDB; R24407. WPI; 92-197392/24. (AJIN) AJINOMOTO KK. 20-SEP-1990; JP-251647. 20-SEP-1990; J04131083-A. Homo sapiens. 30-NOV-1992 (first entry) for cell surface receptors (allowing selective targetting); they anti-proliferative and immune regulating actions plasmid transformed bacteria, with improved antiviral, New modified human beta interferon polypeptide(s) - prepd. by P-PSDB; P50032. INFs of the invention are more active and have different affinities (SEAR) SEARLE G D & CO 17-MAY-1985; 105750 [7-MAY-1984; GB-012564. is used for diagnosis and treatment of cystine-associated 15 bytbggnttyytbcarmgdwnnwnnaaytty 45 ~ 4 gttcctattcNNNNNNNgtataggaacttc 34 aagttcctattcNNNNNNNgtataggaactt 33 19; 7 and cystine diseases. 1561 BP; 251647. Conservative Conservative Location/Qualifiers 230..830 Porter AG; 474 A; = = = = Score 14; DB 4; Pred. No. 3.13e+01 9; Pred. No. 3.13e+01; 0; Mismatches Mismatches 342 C; DB 3; 337 Length 1561; 15; Length 501; ę, Indels Indels 408 <u>;</u> <u>;</u> Gaps Gaps and 0 ç

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Q47839 standard; Q47839;

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Human interleukin 9 receptor clone ph9RA6.

l6-MAR-1994 (first entry)

ID ACC DIT FITTER FOR KWARP FITTER FITTER FOR KWARP FITTER F સ В Matches Query Match Best Local Similarity 1171 cctctacagtgtacacaatgggaacttc 1198 cytokine. Nucleic acid encoding interleukin-9 receptor - used to reagents used in diagnosis and therapy involving interl 01-SEP-1994. 25-FEB-1994; G00373. /product= Chloramphenicol acetyltransferase WO9419472-A. S 21-APR-1995 (first entry) Q71367 standard; DNA; 3249 Sequence expression of the IL-9 receptor protein and to probe for the IL-9 produce IL-9 receptor or as probes for cells which respond to the Claim 6; Page 18; 30pp; English. The interleukin (IL) 9 receptor nucleic acid sequence can be used WPI; 93-303390/38. Homo sapiens. Interleukin 9 receptor; IL-9; /label= 2mu replication region. misc feature 2375..2666 /*tag= misc_signal Synthetic. 2 mu plasmid; fermentation; Cassette; gene expression; promoter; recombinant protein; E.coli/S.cerevisiae shuttle vector pMTL8100. Q71367; IL-9 receptor levels. to the receptor and for qualitative and quantative measurement of the IL-9 receptor can be used therapeutically to block IL-9 binding IL-9 receptor agonists and antagonists. Antibodies directed against coding sequences. Transfected cell lines can be used to screen for Druez C, 09-MAR-1992; US-847347. 25-FEB-1993; U01720. NO9318047-A. /*tag= a /product= Interleukin 9 receptor. antagonist; ss /label= STB locus /*tag= (LUDW-) LUDWIG INST CANCER RES. 16-SEP-1993. tag= 28 cctatacNNNNNNNngaataggaacttc 1 n Renauld J, The complementary sequences can be used to inhibit the 1997 BP; Conservative Ġ. heterologous Location/Qualifiers 3003..3225 461..1117 188..1798 Location/Qualifiers 53.8%; 60.7%; Van Snick J; 388 A; gene; BP. Pred. No. Score 14; <u>.</u> antibodies; therapy; probe; agonist; Mismatches 612 C; clone; cloning; yeast; bacteria; 3.13e+01DB 8; 593 G; Length 1997; interleukin Indels 404 T; produce <u>.</u> 9R Gaps ç 0

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pMTLCJ was constructed essentially by cloning a 0.8 kb BamHI fragment encoding chloramphenicol acetyltransferase (cat) from plasmid pCM4 (Close and Rodriguez, 1982) into the BamHI site of MIJmp8. Single stranded DNA prepared from the resulting recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encompassing the replication region of plasmid pMTL4 (Chambers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                origin of replication and STB locus of the 2mu plasmid, from pl
pVT100-U and inserting it into the unique EcoRV site of pMTLCJ.
New promoter DNA with unique SspI site at gene start position—
esp modified yeast promoter, provides high level of recombinant
protein expression in bacteria and yeast
                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                               misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                  E.coli/S.cerevisiae shuttle vector pMTL8000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the modified cat gene excised as a 0.8 kb BamHI fragment, which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 constructed by isolating a 1.4kb RsaI fragment which encompassed the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  esp modified yeast promoter, provides high level of recombinant
                                                  WPI; 94-294335/36.
                                                               (PUBL-) PUBLIC HEALTH LAB
Faulkner JDB, Minton NP;
                                                                                                 26-FEB-1993; GB-003988.
                                                                                                                25-FEB-1994; G00373
                                                                                                                                  01-SEP-1994.
                                                                                                                                                  WO9419472-A.
                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                Cassette; gene expression; promoter; recombinant protein;
                                                                                                                                                                                                                                                                                                                                                                                                                   21-APR-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Q71366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 al., 1988),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    then blunt ended and ligated to a l.lkb SspI/DraI fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  stranded DNA of the mutated M13 recombinant was then prepared and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to eliminate restriction sites from the cat structural gene. Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 was then used as a template in successive site directed mutagenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasmid as well as those of a S.cerevisiae plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This shuttle vector has the replicative functions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 3; Page 32-34; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein expression in bacteria and yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New promoter DNA with unique SspI site at gene start position -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 94-294335/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Faulkner JDB,
                                                                                                                                                                  /product= Beta
                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                   /label=
                                                                                                                                                                                                                                                                 /label= 2mu replication region
                                                                                                                                                                                                                                                                                                                                                                  termentation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PUBL-) PUBLIC HEALTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 ttctagctagagaataggaacttc 126
                                                                                                                                                                                                                                                                                                                                                  mu plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 ttcNNNNNNngtataggaacttc 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 53.8%;
Local Similarity 62.5%;
                                                                                                                                                                                n
                                                                                                                                                                                                                   STB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3249 BP;
                                                                                                                                                                                                                   locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to give pMTLCJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GB-003988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                     œ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minton NP;
                                                                                                                                                                                                                                                                                                                                                                  heterologous gene; clone; cloning; yeast; bacteria;
                                                                                                                                                                    lactamase.
                                                                                                                                                                                                                                                                                                  Location/Qualifiers 3154..3376
                                                                                                                                                                                                    444..1304
                                                                                                                                                                                                                                                   2526..2817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 882 A;
                                                                                   SERVICE BOARD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 14;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   693 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOARD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No. 3.13e+01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 12; Length 3249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   743 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   931 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The vector was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  trom plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E.coli
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32

RESULT RESULT OF COMMENT OF COMME Ş 밁 Query Match Best Local S exon exon hybridisation; lower organism; structural homologue; Alzheimer's disease; cell death gene; PCR; polymerase chain reaction; ciona intestinalis; echinoderm; lamprey; puffer fish; pVT100-U and inserting it into the unique EcoRV site of pMTLJ. Plasmid pMTLJ was derived from pMTL4 (Chambers at al., 1988), exon /*tag= exon exon exon exon ced-4 Q49264 standard; DNA; 4093 BP. directed mutagenesis method. eliminating the SspI restriction site using the plasmid site origin of replication and STB locus of the 2mu plasmid, from plasmid constructed by isolating a 1.4kb RsaI fragment which encompassed the plasmid as well as those of a S.cerevisiae plasmid. used to identify DNA that codes for evolutionary conserved WPI; 93-336943/42. 01-APR-1992; US-861458. (CAMB-) CAMBRIDGE NEUROSCIENCE INC. 01-APR-1993; U03102. W09320237-A. /*tag= exon /*tag= Caenorhabditis briggsae. Q49264; This shuttle vector has the replicative functions of an E.coli Example 3; Page Disclosure; Fig 8; aminoacid sequences P-PSDB; R42742. Johnson CD, 14-0CT-1993. /*tag= Long-distance homology; evolution; nematode; 28-APR-1994 (first entry) Long-distance homology cloning of genes from lower organisms /*tag= /*tag= /*tag= /*tag= /*product= /*tag= 103 ttctagctagagaataggaacttc 126 11 ttcNNNNNNngtataggaacttc 34 closure; Fig 8; 188pp; English.
primers/probes (Q49266-Q49295) are used to isolate the ced-4 h 53.8%; Similarity 62.5%; ρ C Ф 15; ced-4 3400 BP; Marchionni MA; Conservative gs. Location/Qualifiers 459..3246 30-32; 48pp; English. 2477.. 986..1081 gene_product 3031..3246 2802..2906 1834..2172 1383..1472 651..1716 .2752 917 A; Score 14; DB 12; Pred. No. 3.13e+01 0; Mismatches 738 C; 787 ç; Length 3400; Indels The vector was 958 1988), by 0 Gaps 0

မ В သို့ ၁၃ May 14 13:50 Matches Query Match 53.8%; Best Local Similarity 58.8%; 3228 gaagttcacatcccaatagctgtataagaatttc 3261 gene from the nematode C. briggsae. /*tag= g /product= repeat_unit
/*tag=_ c SIVmac239 nef-deletion. Q24802; Q24802 standard; Simian immunodeficiency virus. PCR; site-directed mutagenesis; retrovirus; Macaque; monkey; polymerase chain reaction; 06-JUL-1992 exon S primer_bind /rpt_type= TERMINAL
/note= "i.e. 5' LTR" /note= "full-length product exon 6528..6597 /product= /product= /*tag= h /*tag= /rpt_type= OTHER
/note= "U3" repeat_unit repeat_region 1..818 /product= tat /*tag= /*tag= /*tag= /product= vif /product= /standard_name= *tag= note= "U5" 'rpt_type= OTHER /*tag= repeat_unit /note= "R" rpt_type= /*tag= /*tag= 34 gaagttcctatacNNNNNNNngaataggaacttc 1 σ 20; 설 ķ ያ gag (first entry) Conservative , LTR. tRNA_PBS 1053..2585 518..600 5340..5984 822..849 601..818 DNA; 6302..6597 6051..6456 5812..6150 2228..5410 Location/Qualifiers 10097 ВP obtained Pred. No. 3.13e+01, Score 14; DB 9; 0; Mismatches 14; à splicing. null mutation; 726 Length 4093; ç Indels 1346 ss. 0 <u>--</u>3 Gaps <u>.</u>

/note= "full-length product obtained by splicing"
CDS 6604..9243

/product= rev

/*tag= l

May 14 13:50 FLP mg 333

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7796

16;

Conservative

0;

FLP.mg Mismatches

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Indels

0; Gaps

0

<u>د</u>

7821

May 14 13:50
Matches 1

Query Match 53.8%; Score 14; DB 3; L Best Local Similarity 61.5%; Pred. No. 3.13e+01; claim 1; Fig 1; 51pp; English.

Parental virus SIVmac239 was isolated from a macaque monkey (see 022487). An SstI fragment of p239SpE3' contg. the C-terminus of the nef gene was cloned into M13 and subjected to site-directed mutagenesis. A 73mer primer was used which was complementary to bases 9215 through 9250 and 9433 through 9469. Since bases 9251 exon exon deletion was confirmed by DNA sequencing. The fragment contq. the deletion was cloned into p239SpE3' to yield p239S-E3' (nef-deletion) which was digested with SphI and ligated to SphI-cut p239SpSp5'. /*tag= GC_signal /*tag= /product= The ligation product was used to directly transfect cultured cells. See also 021075-8. not included in the newly synthesised negative strand. Successful through 9432 were not included in the primer, their complement was producing vaccine Primate lentivirus vaccine protecting against AIDS - and primate lentiviruses and their DNA clones contg. null mutations, useful for P-PSDB; R22365-R22371, R24126-7. Desrosiers RC. WPI; 92-056816/07. polyA_signal GC_signal GC_signal GC_signal misc_signal /rpt_type= TERMINAL
/note= "i.e. 3' LTR /*tag= 10-JUL-1991; U04884. 12-JUL-1990; US-551945. NO9200987-A. [ATA_signal /standard /*tag= /standard /standard repeat_region /product= nef /note= "see /product= rev /note= *see /product= (HARD) HARVARD COLLEGE 23-JAN-1992. /*tag= standard/ /*tag= standard/ /*tag= /*tag= /*tag= /*tag= o /*tag= ש Þ Ħ tat env _name= name= name= _name= 10097 above" above* LTR" 415..424 NF Kappa 429..438 Spl_binding_site 462..471 Spl_binding_site 451..460 Spl_binding_site 440..449 9950..9955 Spl_binding_site 488..494 9280..10097 8803.,9059 8803..8902 9077..9686 ₽₽; 3387 A; 1911 C; The fragment contg. the Length 10097; 2527 G;

primer_bind
/*tag= e /product= CDS repeat_unit /*tag=_d /rpt_type= (
/note= "U3" repeat_unit
/*tag= b IT 43 Q22487 standard; DNA; 10279 BP exon exon exon /*tag= Macaque; monkey; mac239; polymerase chain reaction; PCR; site-directed mutagenesis; retrovirus; ss. 06-JUL-1992 (first entry) /product= /*tag= /rpt_type= OTHER /note= "U5" /rpt_type= TERMINAL
/note= "i.e. 5' LTR repeat_region /*tag=_a Simian immunodeficiency virus SIVmac239 proviral genome. Q22487; /product= tat /product= /*tag= /product= rev /*tag= /note= "full-length product obtained by splicing" /product= tat /*tag= /product= /*tag= /product= /*tag= /product= gag /*tag= f standard_name= /note= "R" rpt_type= *tag= repeat_unit tag= note= *full-length product obtained by splicing* 6604..9243 = * 5 Q Ħ env ŽÍ. g 뒃 Ğ OTHER OTHER tRNA_PBS 1053..2585 LTR. 1..818 601. 1..517 518..600 822..849 8803..8902 6528..6597 6302..6597 5812..6150 5340..5984 6051..6456 2228..5410 Location/Qualifiers

exon

above"

8803..9059

SG

note= "see /product= /*tag= /note= "see

above"

9077..9868

rev

May 14 13:50

FILP,mg

36

0

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characteristic of SIV infection were co-cultivated with HuT-78 cells. Infectious SIVmac239 virus was identified in the cell supernatant. Total cell DNA was prepared from SIVmac239-infected cells and digested with EcoRI. An EMBL-4 library was constructed from 10-20kb EcoRI fragments (EcoRI is a non-cutter of SIVmac239). The library was screened with pK2 BamA as probe and a full-length molecular clone was isolated and sequenced. Then, EMBL-SIVmac239
                                                                                                                                                                                                                                                                                                                                                                                                                                                       polyA_signal
/*tag= x
                                                                                     In a separate reaction, EMBI-SIVmac239 was digested with EcoRI SphI. A 6361bp fragment from viral nucleotide 6452 to the EcoRI
                                                                                                                                                                                                                                                                          Disclosure; Fig 1; 51pp; English.
                                                                                                                                                                                                                                                                                                       Primate lentivirus vaccine protecting against AIDS - and primate lentiviruses and their DNA clones contg. null mutations, useful i
                                                                                                                                                                                                                                                                                                                                                      WPI; 92-056816/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GC_signal
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nef-deletion mutant. See also Q21075-8.
Sequence 10279 BP; 3465 A; 1936 C;
                                          generate the full-length genomic sequence and to produce the
                                                                        site in the right flanking cellular sequence, was inserted in
                                                                                                                                                                                                                                                              Cell-free serum samples from a macaque monkey exhibiting symptoms
                                                                                                                                                                                                                                                                                            producing vaccine
                                                                                                                                                                                                                                                                                                                                    P-PSDB; R22365-R22372, R24126.
                                                                                                                                                                                                                                                                                                                                                                  Desrosiers RC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_type= TERMINAL
/note= "i.e. 3' LTR
                             preferred null-mutations of the invention. See Q24802
                                                         pBS(-) to produce subclone p239SpE3'. These subclones were used to
                                                                                                                   6451, was inserted in vector pBS(+) to produce subclone p239SpSp5/
                                                                                                                               in the left flanking cellular DNA sequence to viral nucleotide no.
                                                                                                                                              was digested with SphI and a 6706bp fragment, contg. the SphI site
                                                                                                                                                                                                                                                                                                                                                                                (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                              10-JUL-1991; U04884.
12-JUL-1990; US-551945.
                                                                                                                                                                                                                                                                                                                                                                                                                           23-JAN-1992.
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429..438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spl_binding_site 488..494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10132..10137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9462..10279
 2569 G;
                              for
                                                                                                                                                                                                                                                                                                           useful for
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Query Match

53.8%;

Score 14;

DB بب

Length 10279;

£ 밁 Matches Best Local /*tag= o
mat_peptide
/** /*tag= a
misc_binding /*tag= q mat_peptide /*tag= p mat_peptide mat_peptide
/*tag= h TATA_signal /*tag= d LT 44 Q54676 exon exon Q54676; exon /*tag= intron /*tag= /*tag= /*tag= 7796 agttcctctactgtaaaatgaattgg 7821 intron /*tag= mat_peptide /*tag= mat_peptide mat_peptide mat_peptide /*tag= mat_peptide /*tag= mat_peptide /*tag= mat_peptide transit_peptide transit_peptide Oryza sativa reverse transcriptase; plaques; ds. Rice; starch; transit peptide; Rice starch 03-AUG-1994 /*tag= /*tag= /*tag= mat_peptide /*tag= /*tag= /*tag= /*tag= transit_peptide CAAT_signal /*tag= promoter /*tag= /*tag= 32 agttcctatacNNNNNNNngaatagg 7 = = = = Þ Ħ standard; DNA; 12151 ъ 4 Ø Similarity 61.5%; 4 c • 16; branching enzyme gene. Conservative (first entry) 5821..5853 9862. 9595. 9019. 8519. 5854..6028 3546..3608 3360..3443 636..335 5821..6028 3609..5820 3546..3608 3444..3545 8245..8361 6648..6917 6144..6231 3291..3296 3221..3225 3164..3172 Location/Qualifiers 3352..3443 10409..10609 10210..10326 1026..7932 .0011..1009 . 9929 .9126 .8581 В₽ Pred. No. 3.13e+01; 0 pectin; Mismatches cereal; aminopectin; 10; Indels 0 Gaps

May 14 13:50

May 14 13:50 FIP:mg

PS Claim 4; Page 10-11; 21pp; Japanese.
CC The sequence shows a gene encoding a branching enzyme of rice starch.
CC The enzyme can be used to modify mainopectin content of starch in
CC cereal particles by introducing the basic sequence into a rice plant.
CC This process can be used to improve the taste of the rice.
CC This process can be used to improve the taste of the rice.
SO Sequence 12151 BP; 3273 A; 2479 C; 2506 G; 3890 T;

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RESULT ID Q6 AC Q6 /*tag= c misc_binding c+ag= b 062137 standard; 062137; /*tag= c TATA_signal Rice starch branching enzyme gene.
Rice starch branching enzyme; oryza sativa; amylopectin; albumen; exon exon exon exon /note= /*tag= /label= /*tag= /*tag= CAAT_signal 07-MAR-1995 /*tag= /*tag= protein. bases 5854-6028 encode a region of the mature /*tag= /label= Intron /*tag= Oryza sativa starch; ss. /label= Intron intron /label= Intron intron /note= "Bases /label= Exon 3. /*tag= /label= Intron intron /note= /label= /*tag= intron /note= /label= Exon promoter *Mature Exon "Transit g Exon "Transit (first entry) n 2. 5821..6028 3546..3608 5821-5853 encode the transit peptide, 4 protein coding region.* 6214..6647 ω peptide coding region."
3609..5820 peptide coding region.*
3444..3545 6144..6213 Location/Qualifiers 636..3351 6029..6143 3352..3443 3291..3296 3221..3225 3164..3172 cDNA to mRNA; 12151 ВP

exon

6648..6917

May 14 13:50 FI.P mg

39

8

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exon exon exon /*tag= /label= /*tag= ар /label= Intron 12. 10210..10326 exon /*tag= v /label= Intron exon exon /*tag= exon /*tag= p /label= Intron /note= "Mature protein coding region." intron 10092..10209 /*tag= intron /note= /*tag= exon /*tag= /*tag= intron note= /label= /label= /label= Intron 11 /*tag= intron /note= /label= Exon 11. /label= Intron /note= "Mature protein coding region." /label= Exon 10 /*tag= /label= Intron /note= "Mature protein coding region."
intron 8582..9018 /label= Intron intron intron /note= /label= Intron /*tag= /note= "Mature protein coding region."
intron 6918..7025 /*tag= m /label= Exon 5. ntron 'label= Exon 8. note= "Mature /label= Exon /label= Exon label= "Mature protein coding region." 10327..10408 *Mature protein coding region. * 9930..10010 "Mature "Mature Exon ae Exon 13. Intron 13. Exon 12. л 9. 9595..9696 л 8. 9019..9126 л 7. 8519..8581 л 6. 8245..8361 1 5. 7026..7932 110. 9862..9929 protein coding region. 9127..9594 protein coding region. 8362..8518 protein coding region. T933..8244 10409..10865 10011..10091 9697..9861

> May 14 13:50 /*tag= ai J06098656-A. 12-APR-1994. 30-MAR-1992; 102500. 30-MAR-1992; JP-102500. polyA_signal /*tag= ah polyA_signal /*tag= ag (MITS-) MITSUI CYOSAI SHOKUBUTSU BIO KENKYUSHO. WPI; 94-155835/19. 3'UTR used to increase the amylopectin content of albumen Claim 1; Page 16-21; 24pp; Japanese. Transgenic rice containing the rice starch branch family enzyme polyA_signal codon. translation termination signal, /note= "Bases 10409-10609 encode a region of mature protein. Bases 10610-10612 are the /*tag= 'label= Exon 14 af 10610..10865 0865..10888 .0839..10842 .0814..10817 i.e. a stop FI.P.mg the

Ş aagttcctattcNNNNNNNgtataggaac 31

밁

9848 aagttccttttcaggttattgtctttgaac 9877

Query Match Best Local S Matches

h 53.8%; Similarity 60.0%;

Score 14; DB 12; Length 12151; Pred. No. 3.13e+01;

18;

Conservative

<u>,</u>,

Mismatches

12; Indels

<u>,</u> Gaps

0;

increasing the content of amylopectin in albumen starch and thus enabling efficient mass production of various proteins. Sequence 12151 BP; 3269 A; 2470 C; 2518 G; 3891 T;

The introduction of the rice starch branch-forming enzyme gene into a rice increase the activity of this enzyme in the plant, thereby

Search completed: Tue May 14 13:59:39 1996 Job time : 56 secs.

Release 2.1D John F. Collins, Biocomputing Research Unit. Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K. Distribution rights by IntelliGenetics, Inc.

MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue May 14 13:59:57 1996; MasPar time 25.23 Seconds 484.494 Million cell updates/sec

Tabular output not generated

N.A. Sequence: Scoring table: Perfect Score: Description: Title: Comp: (1-34) from frt.seq 26 ¥ï₽ 1 gaagttcctattcNNNNNNNgtataggaacttc 34 cttcaaggataagNNNNNNNCatatccttgaag

TABLE default Gap 10

Searched: STD : 518261 seqs, 179750453 bases x 2 Dbase 0; Query 0

Post-processing: Minimum Match 0% Listing first 45 summaries

15:EST15 16:EST16 17:EST17 18:EST18 19:EST19 20:EST20 21:EST21 22:EST22 23:EST23 24:EST24 25:EST25 26:EST26 27:EST27 28:EST28 29:EST23 24:EST24 25:EST25 26:EST26 27:EST27 28:EST28 29:EST29 30:EST30 31:EST31 32:EST33 33:EST33 34:EST34 35:EST35 36:EST36 37:EST37 38:EST38 39:EST39 40:EST40 41:EST41 42:EST42 43:EST43 44:EST44 45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST50 51:EST51 52:EST55 53:EST53 54:EST54 55:EST55 56:EST56 57:EST57 58:EST55 59:EST59 60:EST60 61:EST61 62:EST68 69:EST69 70:EST70 71:EST71 72:EST72 73:EST73 74:EST74 75:EST75 76:EST76 77:EST78 78:EST88 79:EST89 80:EST80 81:EST88 84:EST88 84:EST88 85:EST88 86:EST86 45:EST45 46:EST46 47:EST47 48:EST48 49:EST49 50:EST55 51:EST51 52:EST52 53:EST53 54:EST54 55:EST55 56:EST55 57:EST57 58:EST58 59:EST59 60:EST60 61:EST61 62:EST66 63:EST63 64:EST64 65:EST65 66:EST66 67:EST67 68:EST66 69:EST69 70:EST70 71:EST71 72:EST72 73:EST73 74:EST71 75:EST75 76:EST76 77:EST77 78:EST78 79:EST79 80:EST88 87:EST88 89:ST51 90:ST52 91:ST53 92:ST54 9:EST9 10:EST10 11:EST11 12:EST12 13:EST13 14:EST14 :EST1 2:EST2 3:EST3 4:EST4 5:EST5 6:EST6 7:EST7 8:EST8

EST-STS-TWO 95:gnEST1 96:gnEST2 97:gnEST3 98:gnEST4 99:gnEST5 100:gnEST6 101:gnEST7 102:gnEST8 103:gnEST9 104:gnEST1 100:gnEST8 103:gnEST1 109:enEST1 105:gnEST1 107:gnEST2 113:enEST3 112:enEST4 113:enEST5 114:enEST6 115:enEST7 116:enEST8 117:enEST9 118:enEST1 119:enEST11 124:enEST16 125:enEST17 126:enEST18 127:enEST19 20:enEST12 121:enEST13 122:enEST14 123:enEST15

Database:

93:STS5 94:STS6

May 14 13:59 FLPrst

Statistics: Mean 6.755; Variance 1.297; scale 5.207

128:enEST20 129:enEST21 130:enSTS1 131:enSTS2 132:enSTS3

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALI GNMENTS

LOCUS	RESULT
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EST	
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DEFINITION ACCESSION

D40544

Rice cDNA,

partial

sequence

(S2602_1A)

S DEFINITION В ORIGIN FEATURES COMMENT May 14 13:59 SOURCE KEYWORDS ACCESSION **TOCUS** RESULT BASE COUNT REFERENCE Best Local Similarity AUTHORS ORGANISM Matches Query Match JOURNAL JOURNAL source 32 ttcctattccctgcaatgtatagg 55 w ym19h09.r1 H14983 Unpublished (1995) Homo sapiens EST. NCBI gi: 776335 High quality sequence stops: 37 Source: IMAGE Consortium, LLNL Washington University School of Medicine WashU-Merck EST Project The WashU-Merck EST Project Trevaskis, E., Unpublished (1995) Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Ma Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; H14983 This clone is available royalty-free through LINL; contact the 4444 Forest Park Parkway, Box 8501, St. Contact: Wilson GDB: G00-403-625 The WashU-Merck EST Project Hillier, L., Clark, N., Dubuque, T., Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Bonaldo. lmail: est@watson.wustl.edu (bases 1 to 462) 99 314 286 1810 314 286 1800 Consortium (info@image.llnl.gov) for further information. Conservative ø /note="human" /clone="31278" /organism="Homo sapiens" ocation/Qualifiers, 462 bp mRNA EST Homo sapiens cDNA clone 48660 5' 61.5%; 126 c Waterston, R., Williamson, A., 쯧 Score 16; DB 39; Pred. No. 9.06e-04 .. • 93 Mismatches p FLP1st 119 t Elliston, K., Hawkins, M., œ Length 438; Louis, MO 1 others Indels Wohldmann, P. Marra, M., <u>.</u> Gaps <u>,</u>

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RESULT
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Best Local Similarity 66.7%;
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                                                                                                                                                                                                                                                                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                        Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 463)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI gi: 879803
                                                                                                            4444 Forest Park Parkway,
                                                                                                                                                                                                                                                    Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R. WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                year old male. Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-GAATTCGGCACGAC-3'; 3' adaptor sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        primer=M13RP1 Rsite1=EcoRI Rsite2=XhoI Normal lung tissue from a 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vector=pBluescript SK- host=SOLR cells (kanamycin resistant)
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Source: IMAGE Consortium, LLNL
                   High quality sequence stops: 252
                                          Email: est@watson.wustl.edu
                                                                   Fax: 314 286 1810
                                                                                           Tel: 314 286 1800
                                                                                                                                   Washington University School of Medicine
                                                                                                                                                             WashU-Merck EST Project
                                                                                                                                                                                  Contact: Wilson RK
                                                                                                                                                                                                                                Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human clone=117434 library=Stratagene lung (#937210)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GDB: G00-421-201
                                                                                                                                                                                                                                                                                                                                                                                                                 Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               5'-CTCGAGTTTTTTTTTTTTTTTT-3'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMAGE Consortium (info@image.llnl.gov) for further information.
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> May 14 13:59 This clone is available royalty-free through LLNL; contact the FLPrst

> > O\

MAGE Consortium

(info@image.llnl.gov) for further information.

RESULT LOCUS 밁 DEFINITION S 밁 ORIGIN FEATURES ORIGIN FEATURES COMMENT REFERENCE SOURCE KEYWORDS ACCESSION BASE COUNT BASE COUNT uery Match 61.5%; Best Local Similarity 63.3%; Matches 10. Matches Best Local Query Match JOURNAL TITLE AUTHORS ORGANISM Matches source source 145 aagttactataatggttggcaaagaggaaattc 177 306 ttecttttcacagggctgtttaggcacttc 335 5 ttcctattcNNNNNNNngtataggaacttc 34 S Oryza sativa Oryza sativa (strain Nipponbare,) Seedling Root cDNA to D24501 Fax: Rice cDNA, NCBI gi: 718335 NCBI gi: 428353 Phone: 0298-38-7441 Japan Submitted (2-NOV-1993) to DDBJ by: Unpublished (1993) group; Charophyta/Embryophyta group; Embryophyta; Magnoliophyta; Liliopsida; Commelinidae; Poales; Poaceae; Oryza. Eukaryotae; mitochondrial eukaryotes; Chlorophyta/Embryophyta EST (expressed sequence tag). RICR2068A 57.7%; Similarity 60.6%; PROJECT ='RGP'. Tsukuba, Ibaraki Kannondai 2-1-2 National Institute of Agrobiological Resources Dept. Rice Genome Research Program Yuzo Minobe Rice cDNA from root Minobe, Y. and Sasaki, T. 19; 20; (bases 1 to 249) 105 86 a 0298-38-7468 Conservative Conservative ø /tissue_type="Root" 1..249 /note="human' /clone="117434" 1..463Location/Qualifiers /sequenced_mol="cDNA to mRNA" /dev_stage="Seedling" /strain="Nipponbare" /organism="Homo sapiens" /organism="Oryza sativa" Location/Qualifiers partial sequence (R2068_1A). 108 с 40 c 249 뤗 Score 16; DB 86; Pred. No. 9.06e-04; Score 15; DB 63; Pred. No. 1.91e-02; ç 100 ç 60 g **□RNA** Mismatches Mismatches g 143 61 t đ <u>;;</u> Length 249; Length 463; EST -1 2 others Indels others 26-MAY-1995 ç ç Gaps Gaps nRNA. ç 0;

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aagttcctatacNNNNNNNngaataggaacttc 1

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RESULT 7 LOCUS DEFINITION ACCESSION KEYWORDS	Db 49 q 0y 1 q	Query Match Best Local Matches	FEATURES source source BASE COUNT ORIGIN		TITLE JOURNAL COMMENT	REFERENCE AUTHORS	ORGANISM	RESULT 6 LOCUS DEFINITION ACCESSION KEYWORDS SOURCE
R07677 288 bp mRNA EST 05-APR-1995 ye98d03.rl Homo sapiens cDNA clone 125765 5'. R07677	gaagttoctattacttcttatgattgggagctt 81 gaagttoctattcNNNNNNNgtataggaactt 33	<pre>ch 57.7%; Score 15; DB 35; Length 288; l Similarity 60.6%; Pred. No. 1.91e-02; 20; Conservative 0; Mismatches 13; Indels 0; Gaps 0;</pre>	NCBI gi: 759600 Location/Qualifiers 1288 /organism="Homo sapiens" /clone="125765" /note="human" 90 a 49 c 45 g 104 t	Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: est@watson.wustl.edu High qality sequence stops: 248 Source: IMAGE Consortium, LLML This clone is available royalty-free through LLML; contact the IMAGE Consortium (info@image.llnl.gov) for further information.	Wilson,R. The WashU-Merck EST Project Unpublished (1995) Contact. Wilson BK	rimdees; Catalinini, nominidae; 1 to 288) 1 to 288) 1, Clark,N., Dubuque,T., Elliston, Hultman,M., Kucaba,T., Le,M., L., Rifkin,L., Rohlfing,T., Soares, E., Waterston,R., Williamson,A.,	ed by Bent ens e; Metazoa Primates:	

May 14 13:59 SOURCE vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B human clone=125765 library=Soares fetal liver spleen INFLS (ampicillin resistant) primer=M13RP1 Rsite1=Pac I Rsite2=Eco RI

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ORGANISM Homo sapiens vector. Library went through one round of normalization. Library I and cloned into the Pac I and Eco RI sites of the modified pT7T3 Liver and spleen from a 20 week-post conception male fetus. 1st strand cDNA was primed with a Pac I - oligo (dT) primer [5' constructed by Bento Soares and M.Fatima Bonaldo. cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac

Eutheria; Primates; Catarrhini; Hominidae; Sucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;

REFERENCE AUTHORS Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Hillier, L., Clark, N., Dubuque, T., (bases 1 to 288) Kucaba, T., Le, M., Lennon, G., Marra, M., Elliston, K., Hawkins, M.,

Unpublished (1995) The WashU-Merck EST Project Wilson, R.

COMMENT JOURNAL

Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. High qality sequence stops: 248 Source: IMAGE Consortium, LLNL WashU-Merck EST Project Contact: Wilson RK ⊡mail: est0watson.wustl.edu

FEATURES source NCBI gi: 759600 /organism="Homo sapiens" /clone="125765" /note="human" 1...288 Location/Qualifiers

BASE COUNT

9

49 c

45

g

104 t

မှ 밁 Matches Query Match 57.7%; Best Local Similarity 60.6%; 49 gaagtteetattaettettatgattgggagett 81 34 gaagttcctatacNNNNNNNngaataggaactt 2 20; Conservative Score 15; DB 35; Length 288; Pred. No. 1.91e-02; 0. Mismatches 13; Indels **.**

Gaps

<u>.</u>

KEYWORDS SOURCE RESULT LOCUS ACCESSION DEFINITION **∞** H41218 EST. yp64e12.sl Homo sapiens cDNA clone 192238 3' similar to contains Alu repetitive element;.
H41218 vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=Promega -21m13 Rsite1=Pac I human clone=192238 library=Soares fetal liver spleen lNFLS Rsite2=Eco RI Liver and spleen from a 20 week-post conception male

BASE COUNT FEATURES REFERENCE ORGANISM Query Match 57.7%; Best Local Similarity 64.3%; Matches JOURNAL AUTHORS 09-JAN-1995 (Rel. 42, 08-SEP-1995 (Rel. 45, source Bult C.J., Lee N., Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Homo sapiens (human) pregnancy-specific (HT:2583). EST79508 Homo sapiens cDNA similar to beta-1-glycoprotein HS41410 Adams M.D., T29414; 1-381224 gaagatccnatacagngataaaaatagg 251 ş gaagttcctatacNNNNNNNngaatagg 7 Homo sapiens NCBI Washington University School of Medicine Unpublished Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Bonaldo. normalization. Library constructed by Bento Soares and M.Fatima digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT/T3 vector. Library went through one round of High quality sequence stops: 58 4444 Forest Park Parkway, Box 8501, St. Louis, WashU-Merck EST Project Contact: Wilson RK The WashU-Merck EST Project Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; This clone is available royalty-free through LLNL; contact the Source: IMAGE Consortium, Email: est@watson.wustl.edu Fax: 314 286 1810 Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), IMAGE Consortium (info@image.llnl.gov) for further information. 18; (bases 1 to 353) standard; RNA; EST; 381 BP Kerlavage A.R., Fleischmann R.D., Fuldner R.A., Lee N., Kirkness E.F., Weinstock K.G., Gocayne J.D., gi: 917270 91 314 286 1800 Conservative ۵u /note="human" /clone="192238" /organism="Homo sapiens" Location/Qualifiers (1995)68 C Last updated, Version 2) Created) Score 15; DB 16; Pred. No. 1.91e-02; .. 74 g Mismatches TIMI 106 t 10; Fuldner R.A., Length 353; 14 others Indels Mammalia; Hominidae. MO 63108 <u>.</u> Gaps <u>.</u>

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SOURCE င္ 밁 REFERENCE KEYWORDS ACCESSION DEFINITION AUTHORS ORGANISM Matches Query Match Query Match 57.7%; Best Local Similarity 64.0%; Fischer C., Hastings G.A., He W.W., Hu J.S., Greene J.M., Gruber J., Hudson P., Kim A., Kozak D.L., Kunsch C., Ji H., Li Meissner P.S., Olsen H., Raymond L., Wei Y.F., Wing J., Xu C., Yu G.L., Ruben S.M., Dillon P.J., Fannon M.R., Rosen C.A., Haseltine W.A., Fields C., Fraser C.M., Venter J.C.; "Initial Assessment of Human Gene Diversity and Expression Patterns Based Upon 52 Million Basepairs of cDNA Sequence"; ERNA Pellegrino S.M., Phillips C.A., Ryder S.E., Scott J.L., Saudek D.M., Shirley R., Small K.V., Spriggs T.A., Utterback T.R., Weldman J.F., Li Y., Bednarik D.P., Cao L., Cepeda M.A., Sequence 611512 source Fax: 3018699423 Email: tdbinfo@tdb.tigr.org For clone availability, Other ESTs: THC24005 Contact: Venter, JC The Institute for Genomic Research 932 Clopper Rd, Gaithersburg, MD 20878 Tel: 3018699056 Unpublished. Coleman T.A., Merrick J.M., MORENO-PALANQUES R.F., McDonald L.A., Nguyen D.T., Kelley J.M., Klimek K.M., Kelley J.C., Liu L.I., Marmaros S.M., Glodek A., Gnehm C.L., FitzGerald L.M., FitzHugh W.M., Fritchman J.L., White O., Sutton G., Blake J.A., Brandon R.C., Chiu M.W., Clayton R.A., Cline R.T., Cotton M.D., Earle-Hughes J., Fine L.D., 313 gaageteetatactacatgtggaat 337 please contact the TIGR Database (tdbinfo@tdb.tigr.org). NCBI gi: additional sequence and expression information related to this EST, 34 10 gaagttcctatacNNNNNNNngaat 10 Kelley,J.M., Klimek,K.M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Clayton,R.A., Cline,R.T., Cotton,M.D., Earle-Hughes,J., Fine,L.D., FitzGerald,L.M., FitzHugh,W.M., Fritchman,J.L., Geoghagen,N.S.M., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle Jr,P.S., Bult, C.J., Lee, N., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Chiu, M.-W., Homo sapiens EST. pregnancy-specific (HT:2583).
T29414 EST79508 Homo sapiens cDNA similar to beta-1-glycoprotein Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; human primer=M13-21 library=Human Placenta. 16; (bases 1 to 381) 381 BP; 107 A; Conservative Collins E.J., Dimke D., Feng P., Ferrie A., /organism="Homo sapiens" /note="human" <1..>381 Location/Qualifiers Shirley, R., Blake J.A., 381 bp Hanna M.C., Hedblom E., Hinkle Jr P.S., 78 C; 71 G; 125 T; 0 other; Score 15; DB 119; Pred. No. 1.91e-02; 0 Small, K.V., Mismatches Brandon R.C., DB 119; Length 381; Spriggs, T.A., Utterback, T.R., 9; Indels Geoghagen N.S.M., Fuldmer, R.A., 06-SEP-1995 <u>,</u>, Gaps <u>.</u>

JOURNAL TITLE source Gruber, J., Hudson, P., Kim, A., Kozak, D.L., Kunsch, C., Ji, H., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.-F., Wing, J., Xu, C., Yu, G.-L., Ruben, S.M., Dillon, P.J., Fannon, M.R., Rosen, C.A., Coleman, T.A., Collins, E.-J., Dimke, D., Feng, P., Ferrie, A., Fischer, C., Hastings, G.A., He, W.-M., Hu, J.-S., Greene, J.M., Other ESTs: THC24005 Unpublished (1995) NCBI gi: 611512 For clone availability, additional sequence and expression information related to this EST, please contact the TIGR Database Contact: Venter, JC Based Upon 52 Million Basepairs of cDNA Sequence Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C. Weidman, J.F., Li, Y., Bednarik, D.P., 932 Clopper Rd, Gaithersburg, MD 20878 The Institute for Genomic Research Initial Assessment of Human Gene Diversity and Expression Patterns (tdbinfo@tdb.tigr.org). Email: tdbinfo@tdb.tigr.org 107 3018699423 3018699056 b <1..>381 /note="human" /organism="Homo sapiens" 1..381 Location/Qualifiers 78 c 71 g 125 t Cao, L., Cepeda, M.A.,

ORIGIN BASE COUNT FEATURES

Query Match 57.7%; Best Local Similarity 64.0%; Pred. No. 1.91e-02; Score 15; DB 70; Length 381;

f 밁 313 gaagctcctatactacatgtggaat 337 34

Matches

16;

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Mismatches

9,

Indels

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Gaps

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RESULT

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06-NOV-1995

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Pocus DEFINITION RESULT 11 R79758 410 bp

KEYWORDS SOURCE ACCESSION R79758 yi89e12.rl Homo sapiens cDNA clone 146446 5'. cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo. EST. obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer (5)(Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13RP1 Rsitel=Not I Rsite2=Eco RI Female placenta human clone=146446 library=Soares placenta Nb2HP vector=pT7T3D

REFERENCE AUTHORS ORGANISM Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Ma Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Hillier, L., Homo sapiens Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 410) Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Marra, M.,

Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and

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COMMENT JOURNAL Contact: Wilson RK Unpublished (1995) The WashU-Merck EST Project

WashU-Merck EST Project 4444 Forest Park Parkway, Box 8501, St. Louis, Washington University School of Medicine Email: est@watson.wustl.edu Fax: 314 286 1810 314 286 1800 MO 63108

FEATURES source NCBI gi: 856039 1..410 Location/Qualifiers

High quality sequence stops: 2 Source: IMAGE Consortium, LLNL

277

This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

ORIGIN BASE COUNT 117 a /note="human" /organism="Homo sapiens" /clone="146446" 82 c 90 g 118 t 3 others

Query Match 57.7%; Best Local Similarity 63.0%; Matches Conservative Pred. No. 1.91e-02 Score 15; 0. Mismatches DB 56; Length 410; Indels <u>.</u> Gaps

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Ş 232 tccacttcgtacttctgtataggaact 258 6 tcctattcNNNNNNNngtataggaact 32 = = = =

SOURCE KEYWORDS ACCESSION DEFINITION Arabidopsis thaliana Lambda PRIL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour darkthale cress clone=200C2T7 primer=T7 dye primer library=Lambda-PRL2 strain=var columbia vector=lambda Zip-Lox Rsitel=Sal Rsite2=Not H76310 H76310 412 bp mRNA EST 18015 Arabidopsis thaliana cDNA clone 200C2T7. primed cDNA. rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo Q.

ORGANISM Brassicaceae; Arabidopsis. Eucaryotae; Embryophyta; Magnoliophyta; Magnoliopsida; Capparales;

REFERENCE AUTHORS Newman, T., de Bruijn, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, (bases 1 to 412)

COMMENT TITLE JOURNAL large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994) Genes galore: a summary of methods for accessing results from

Michigan State University Contact: Thomas Newman MSU-DOE-PRL, Michigan State University,Plant Biology Bldg.,E. MSU-DOE Plant Research Laboratory

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RESULT
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                                                                                                                                                                                                         Sequence 412 BP; 103 A; 83 C; 84 G; 126 T; 16 other;
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10-NOV-1995 (Rel. 45, Last upd
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Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ib
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Ohlrogge J., Raikhel N., Somerville S., Thomas
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                                                                                                               Query Match 57.7%;
Best Local Similarity 62.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
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                        414 gttccttttgtgatttctgtatagggact 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           yd77q07.rl Homo sapiens cDNA clone 114300 5' similar to
SP:UBC5_DROME P35128 UBIQUITIN-CONJUGATING ENZYME E2-17 KD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pTTT3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T86566
                                                                                                                                                                                                                                                                                                                                 NCBI gi: 714918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-Merck EST Project Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human clone=114300 library=Soares fetal liver spleen 1NFLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T86566
                                                                                                                                                                                                                                                                                                                                                                                                                          Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria; Primates; Catarrhini; Hominidae;
                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                                MAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stops: 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ≧mail: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ampicillin resistant) primer=M13RP1 Rsite1=Pac I Rsite2=Eco RI
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                                                                                                                                                                                                                          /note="human"
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Pred. No.
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6862 Arabidopsis thaliana cDNA clone 121G9T7.

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Best Local Similarity 64.5%;
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                                        Dilleniidae; Capparales; Brassicaceae
                                                              Eukaryota; Plantae; Embryobionta; Magnoliophyta; Magnoliopsida;
                                                                                      Arabidopsis thaliana
                                                                                                                               6862 Arabidopsis thaliana cDNA clone 121G9T7.
                                                                                                                                                                           03-FEB-1995
                                                                                                                                                                                                T43599;
                                                                                                                                                     03-FEB-1995 (Rel. 42, Created)
10-NOV-1995 (Rel. 45, Last upd
                                                                                                                                                                                                                                                                                                                                                       19
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                                                                                                                                                                                                                                                                                                       agttcctattcNNNNNNngtataggaactt 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vector=lambda Zip-Lox primer=T7 dye primer Rsite1=Sal Rsite2=Not Lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The mRNA sources were 1) 7 day germinated etiolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 517-353-0854
Fax: 517-353-9168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genes galore: a summary of methods for accessing results from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                with 24 hour light cycle, half on 16 hr light, 8 hour dark-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seedlings; 2) tissue culture grown roots; 3) staged plants half
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thale cress clone=121G9T7 library=Lambda-PRL2 strain=var columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: 22313tcn@ibm.cl.msu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Michigan State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Thomas Newman
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Sequence 452 BP; 116 A; 69 C; 115 G; 130 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 State University MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E. Lansing, Mi Tel: 517-353-0854 Fax: 517-353-9168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22313tcn@ibm.cl.msu.edu. NCBI gi: 947993
                                           Contact: Wilson RK
WashU-Merck EST Project
                                                                                                                                                                                                                                                          Hillier, L., Clark, N., Dubuque, T.,
                                                                                                                                                                                                                                                                                                                             Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
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R53335
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St.
                                                                                                                               Unpublished
                                                                                                                                                                                                                    Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDB: G00-412-467
                                                                                                                                                                                          Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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                                                                                                                                                    The WashU-Merck EST Project
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                                                                                                                                                                                                                                                                                                       Eutheria; Archonta; Primates;
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Ohlrogge J., Raikhel N.,
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/clone="121G9T7"
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Pred. No. 1.91e-02;
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   Louis, MO 63108
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Best Local Similarity 64.0%;
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EST.
                                                                                                                                                                                                                 Unpublished (1995)
                                                                                                                                                                                                                                                                                                         Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yul8q03.rl Homo sapiens cDNA clone 234196 5' similar to gb:S52450 NONSPECIFIC LIPID-TRANSFER PROTEIN PRECURSOR (HUMAN);.
                                                                        Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                             Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I and cloned into the Pac I and Eco RI sites of the modified pT7T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
                                                                                                                   Washington University School of Medicine
                                                                                                                                           WashU-Merck EST Project
                                                                                                                                                                   Contact: Wilson RK
                                                                                                                                                                                                                                         The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                 Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 487)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vector. Library went through one round of normalization. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            host=DH10B (ampicillin resistant) Rsitel=Pac I Rsite2=Eco RI Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human clone=234196 primer=M13RP1 library=Soares fetal liver spleen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Source: IMAGE Consortium,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                       Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and spleen from a 20 week-post conception male fetus. 1st strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1NFLS vector=pT7T3D (Pharmacia) with a modified polylinker
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quality sequence stops:
                                                                                             Forest Park Parkway, Box 8501, St. Louis,
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Pred. No. 1.91e-02;
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        Query Match 57.7%;
Best Local Similarity 64.0%;
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Best Local Similarity 64.0%;
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                                                              Sequence 487 BP; 140 A; 93 C; 109 G; 144 T; 1 other;
                                                                                BNA
                                                                                                                                                                                                                                                         Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:
                                                                                                                                                source
                                                                                                                                                                                                                           est@watson.wustl.edu High quality sequence stops: 379 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL
                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                        Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,
                                                                                                                                                                                                                                                                                                                                                                    Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,
                                                                                                                                                                                                                                                                                                                                                                                    Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae
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                                                                                                                                                                                           Information. NCBI gi: 1024998
                                                                                                                                                                                                            contact the IMAGE Consortium (info@image.llnl.gov) for further
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                Score 15; DB 116;
Pred. No. 1.91e-02;
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Pred. No. 1.91e-02;
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                               Length 487;
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KEYWORDS

ACCESSION DEFINITION

Human colon 3'directed MboI cDNA, HUMGS04157, clone cm1934.

18-JUN-1994

Tocas

HUMGS04157

138 bp

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Best Local Similarity 58.1%;
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                                                                                                                                                                                                                                HSGS04157 standard; RNA; EST; 138 BP.
D25789;
23-JUN-1994 (Rel. 40, Created)
27-NOV-1995 (Rel. 45, Last updated, Version 2)
Human colon 3'directed MboI cNA, HUMCS04157, clone cm1934.
                                                                                                 Okubo K., Itoh K., Yoshii J., Yokouchi H.,
                                                                                                                                                         Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae
                                                                                                                                                                                                                 colon; endothel; EST(expressed sequence tag); gene signature(GS).
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Okubo K., Yoshii J., Yokouchi H., Kameyama M.,
                                                         random cDNA sequencing analysis";
                                                                                                                                                                                               Homo sapiens (human)
                                         Unpublished.
                                                                          Okubo K., Itoh K., Yoshii J., Yokouchi H., Matsubara K.;
"Global analysis of gene expression in colon mucosa: a large scale
                                                                                                                   1-138
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Unpublished (1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Okubo, K., Itoh, K., Yoshii, J., Yokouchi, H. and Matsubara, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Suita, Osaka, 565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
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23 c 28 g 36 t
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/sex="male"
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Pred. No. 3.47e-01;
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Query Match 53.8%;
Best Local Similarity 58.1%;
Matches 18; Conservative
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Best Local Similarity 58.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (22-Nov-1993) to DDBJ by: Kousaku Okubo Institute for Molecular and Cellular Biology Osaka University 3-1, Yamadaoka Suita, Osaka, 565 Japan Phone: 06-877-5111 Fax: 06-875-1922
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                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (22-Nov-1993) to DDBJ by: Kousaku Okubo
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                                                                                                                                                                                                                                                                                       Japan
Phone: 06-877-5111
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BP; 45 A; 23 C; 28 G; 36 T; 6 other;
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                                                                                       /tissue_type="colon mucosa"
23 c 28 g 36 t
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/sex="male"
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                                                                                                                          /sequenced_mol="cDNA to mRNA"
/sex="male"
                                                                                                                                                           /organism="Homo sapiens"
/dev_stage="adult"
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Pred. No. 3.47e-01
                Score 14; DB 32;
Pred. No. 3.47e-01
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23

DEFINITION TOCOS S 밁 ORIGIN BASE COUNT FEATURES COMMENT REFERENCE KEYWORDS ACCESSION DEFINITION POCOR RESULT එ KEYWORDS ACCESS ION RESULT Query Match 53.8%; Best Local Similarity 57.7%; AUTHORS JOURNAL ORGANISM source 96 ctnttcaagaaccagtntgggaactt 121 32 8 24 23 ctattcNNNNNNNngtataggaactt 33 H07743 1 (bases 1 to 162)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., yb47e03.s1 Homo sapiens clNA clone 74332 3' 40S RIBOSOMAL PROTEIN S18 (HUMAN). Unpublished (1995) EST. rape library=BNL1 strain=cv. Naehan vector=pT7T3D host=NM522 primer=M13 forward Rsitel=NotI Rsite2=EcoRI Poly(A)-mRNA was EST. NCBI gi: 657167 High qality sequence starts: 1 High qality sequence stops: 1 WashU-Merck EST Project Homo sapiens unidirectionally. Primer: Oligo dT. Average insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence: 5'-GAATTCGGCACGAG-3'; 3' adaptor sequence: 5'-CTCGAGTTTTTTTTTTTTTTTTTTTTTTTTT.3'. human clone=74332 library=Stratagene fetal spleen (#937205) Source: IMAGE Consortium, LINL free through LINL; contact the Email: est@watson.wustl.edu Tel: 314 286 1800 Fax: 314 286 1810 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Washington University School of Medicine WashU-Merck EST Project Contact: Wilson RK Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. primer=-21m13 Rsite1=EcoRI Rsite2=XhoI Pooled fetal spleens. Cloned vector=pBluescript SK- host=SOLR cells (kanamycin resistant) khkh116 H07743 15; Eutheria; Primates; Catarrhini; Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; IMAGE Consortium (info@image.llnl.gov) for further information. 3 Conservative Brassica napus ø /note="human' /clone="74332" /organism="Homo sapiens" 1..162Location/Qualifiers 37 c ģ Score 14; DB 77; Pred. No. 3.47e-01; <u>.</u> 32 CDNA 3'. BNA g Mismatches 49 t Hominidae; Length 162; EST 13 others Ношо. Indels similar to gb:X69150 08-FEB-1995 **.** <u>.</u>.

£ 밁 May 14 13:59 ORIGIN BASE COUNT COMMENT REFERENCE FEATURES Matches Query Match 53.8%; Best Local Similarity 58.8%; ORGANISM JOURNAL AUTHORS 15-NOV-1995 (Rel. 45, Created)
15-NOV-1995 (Rel. 45, Last updated, Version 1)
yu86e09.s1 Homo sapiens cDNA clone 240712 3' similar to gb:L11244
C4B-BINDING PROTEIN BETA CHAIN PRECURSOR (HUMAN);. est@watson.wustl.edu High quality sequence stops: 59 Source: IMAGE Consortium, LINL This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M., Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F., Trevaskis E., Waterston R., Williamson A., Wohldmann P., Wilson R.; School of Medicine 4444 Forest Park Parkway, Box 85 MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: Contact: Wilson RK WashU-Merck EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Unpublished. Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae H78142; HS142226 source Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M., 1-240 Homo sapiens (human) "The WashU-Merck EST Project"; 130 gaagttcccagacttcagttcgagttagaacctc 163 34 gaagttcctatacNNNNNNNngaataggaacttc 1 Unpublished (1995) Brassica napus Sohn, U., Lee, C.M., NCBI gi: 872565 Fax: 0539555327 Tel: Contact: Uik Sohn constructed from the mRNAs by oligo(dT) priming and directionally cloned from the NotI site in the vector pT7T3D purified from EST is putatively homologous to Email: usohn@bh.kyungpook.ac.kr Kyungpook National University Laboratory of Molecular Biology 20; Capparales; Brassicaceae; Brassica. Eucaryotae; Embryophyta; Magnoliophyta; Magnoliopsida; Dilleniidae; (Pharmacia) to the EcoRI site. (bases 1 to 226) standard; RNA; EST; . of Genetic Eng., Kyungpook National Univ., Taegu 702-701, Korea 0539505382 61 Conservative മ 1..226 /strain="cv. Naehan" /note="rape" /organism="Brassica napus" Location/Qualifiers 45 c the Cho, K.H., Jeon, Y.H., Hahn, T.R. and Nam, H.G leaf Score 14; DB 6; Pred. No. 3.47e-01 <u>.</u> 66 g 240 BP. = = = of B.napus. Mismatches 54 unknown 14; Length 226; CDNA gene. Indels library Hominidae 0 Gaps 9

information.

gi: 1056231

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ACCESSION yul0e03.sl Homo sapiens cDNA clone 233404 3' similar to gb|M87942|HUMAALJ83 Human carcinoma cell-derived Alu RNA transcript, (IRNA); gb:X62078 GANGLIOSIDE GM2 ACTIVATOR PRECURSOR H79813 (HUMAN); contains Alu repetitive element;. 09-NOV-1995

KEYWORDS SOURCE cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library human clone=233404 primer=Promega -21m13 library=Soares fetal liver constructed by Bento Soares and M.Fatima Bonaldo. and spleen from a 20 week-post conception male fetus. 1st strand host=DH10B (ampicillin resistant) Rsite1=Pac I Rsite2=Eco RI Liver spleen INFLS vector=pT7T3D (Pharmacia) with a modified polylinker

ORGANISM Homo sapiens Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;

REFERENCE AUTHORS JOURNAL Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Unpublished (1995) Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., The WashU-Merck EST Project Wilson, R. Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and (bases 1 to 265)

COMMENT

High quality sequence stops: 231 Tel: Washington University School of Medicine WashU-Merck EST Project Contact: Wilson RK This clone is available royalty-free through LLNL ; contact the Source: IMAGE Consortium, LLNL Email: est@watson.wustl.edu IMAGE Consortium (info@image.llnl.gov) for further information ax: 314 286 1810 Forest Park Parkway, Box 8501, St. Louis, 314 286 1800 MO 63108

NCBI gi: 1057902 Location/Qualifiers

FEATURES

May 14 13:59 FLPrst

24

ORIGIN BASE COUNT source 91 ຄ <1..>265 /organism="Homo sapiens" /clone="233404" /note="human" 50 c 57 g 60 t

Matches Best Local Query Match 53.8%; Similarity 68.2%; 15 Conservative Pred. No. 3.47e-01 Score 14; 0; Mismatches DB 102; Length 265; Indels 0; Gaps

0

217 cacagntttgtataggaacttc 238

Gaps

0:

Ş 13 cNNNNNNNgtataggaacttc 34

ACCESSION DEFINITION TOCOS SOURCE KEYWORDS RESULT 27 vector=Lafmid BA host=E. coli primer=M13 Forward (Universal) Rsite1=Not I Rsite2=Hind III Size-selected cDNA from polyA+ RNA from human brain. 3-month old neonate.This library is the result of seq1023 Homo sapiens cDNA clone b4HB3MA-COT8-HAP-Ft57 3'. T10038 an attempted normalization of library b4HB3MA. human clone=b4HB3MA-COT8-HAP-Ft57 library=b4HB3MA Cot8-HAP-Ft EST. T10038 300 bp

REFERENCE ORGANISM Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Homo sapiens Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 300)

TITLE AUTHORS JOURNAL Unpublished (1993) Efstratiadis, A. Soares, M.B., Construction and characterization of a normalized cDNA library de Fatima Bonaldo, M., Jelenc, P., Long Su, L.L. and

COMMENT Contact: Bento Soares Department of Psychiatry, 722 W 168th Street, Unit #41, New York, NY Columbia University Email: cuc@cuccfa.ccc.columbia.edu Fax: 2127955886 Tel: 2129602313

ORIGIN FEATURES BASE COUNT source NCBI gi: 471389 103 a /note="human" /clone="b4HB3MA-COT8-HAP-Ft57" /organism="Homo sapiens" Location/Qualifiers 53 c 51 g 93 t

Matches Query Match 53.8%; Best Local Similarity 61.5%; 186 cctattcttgcacaggaataggacct 211 16; Conservative Score 14; DB 66; Pred. No. 3.47e-01 0; Mismatches DB 66; Length 300; 10; <u>.</u> Gaps

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S -1 cctattcNNNNNNngtataggaact 32

RESULT LOCUS 28 HSC1SD111 306 bp RNA EST

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May 14 13:59 FLP.181

26

SOURCE SDO S FEATURES COMMENT REFERENCE ACCESSION DEFINITION SOURCE KEYWORDS ACCESSION DEFINITION RESULT BASE COUNT **EYWORDS** AUTHORS ORGANISM ORGANISM Matches Query Match 53.8%; Best Local Similarity 59.4%; JOURNAL source 254 aaattcctaatctgttttttctatagggcctt 285 2 aagttcctattcNNNNNNNgtataggaactt 33 မ္တ Parsons,J., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rikkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R. Wash-Merck EST Project G11665 Homo sapiens EST. T98116 ye30b04.rl Homo sapiens Homo sapiens 4444 year old male. Cloned unidirectionally. Primer: Oligo dT. Average insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence: vector=pBluescript SK- host=SOLR cells (kanamycin resistant) G11665 human STS WI-10042. NCBI gi: 747461 Tel: Contact: Wilson RK Unpublished (1995) primer=M13RP1 Rsite1=EcoRI Rsite2=XhoI Normal lung tissue from a 72 human clone=119215 library=Stratagene lung (#937210) repetitive element ;. Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata; human STSs derived from random genomic DNA. STS sequence; primer; sequence tagged site. This clone is available royalty-free through LLNL; contact the Washington University School of Medicine WashU-Merck EST Project 5'-GAATTCGGCACGAG-3'; 3' adaptor sequence: Catarrhini; Hominidae; Homo. 19; IMAGE Consortium (info@image.llnl.gov) for further information. Source: IMAGE Consortium, LLNL High quality sequence stops: Email: est@watson.wustl.edu Eutheria; Primates; Catarrhini; Hominidae; Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; 5'-CTCGAGTTTTTTTTTTTTTTTTT-3'. (bases 1 to 309) 314 286 1810 88 314 286 1800 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Conservative ىھ /note="human" /organism="Homo sapiens" /clone="119215" 1..309 Location/Qualifiers 75 c 326 bp Pred. Score 14; DB 88; Pred. No. 3.47e-01 0; **3**5 cDNA clone 119215 5' DNA Mismatches Ω 110 t Length 309; STS 1 others Ношо. Indels similar 19-0CT-1995 <u>.</u> ç Gaps contains 0 드

1 (bases 1 to

27

23

Whitehead Institute/MIT Center for Genome Research; Physically

AUTHORS TITLE JOURNAL

Unpublished (1995)

Mapped STSs

Hudson, T.

REFERENCE

(bases 1 to 347)

AUTHORS TITLE JOURNAL

Direct Submission

Parmentier, Y., Criqui, M.C., Durr, A. and Fleck, J.

Submitted (15-SEP-1994) to the EMBL/GenBank/DDBJ databases. GDR-1003 ACS, INRA, laboratoire de Biologie Moleculaire, BP

BP 27,

TOCUS FEATURES COMMENT SOURCE KEYWORDS May 14 13:59 SOURCE KEYWORDS DEFINITION RESULT BASE COUNT REFERENCE ACCESSION ACCESSION ORGANISM Matches Query Match 53.8%; Best Local Similarity 58.8%; JOURNAL AUTHORS ORGANISM source 203 gaagtgccttctcacactctggtttgggagcttc 236 1 gaagttcctattcNNNNNNNgtataggaacttc 34 32 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. WashU-Merck EST Project Arabidopsis thaliana Primer: Oligo dT. Hepatectomy from normal 49 year old male caucasian. Average insert size: 1.1 kb; Uni-ZAP XR Vector; 5' adaptor sequence: 5'-GAATTCCGCACGAG-3'; 3' adaptor sequence: human clone=61440 library=Stratagene liver (#937224) vector=pBluescript SK host=SOLR cells (kanamycin resistant) primer=-21ml3 Rsitel=EcoRI Rsite2=KhoI Cloned unidirectionally. EST. Homo sapiens T40922 Eukaryotae; mitochondrial eukaryotes; Chlorophyta/Embryophyta group; Charophyta/Embryophyta group; Embryophyta; Magnoliophyta; A. thaliana transcribed sequence; clone FAFM89 Other_ESTs: yal4c01.r2 Unpublished (1995) thale cress. expressed sequence tag; partial cDNA sequence Z37189 ATTS3932 NCBI gi: 648505 5'-CTCGAGTTTTTTTTTTTTTTTTT-3'. SP:C4BB_HUMAN P20851 C4B-BINDING PROTEIN BETA CHAIN ,. Magnoliopsida; Dilleniidae; Capparales; Brassicaceae; Arabidopsis. 20; This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Source: IMAGE Consortium, LLNL mail: est@watson.wustl.edu Tel: 314 286 1800 Fax: 314 286 1810 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Washington University School of Medicine WashU-Merck EST Project Contact: Wilson RK Sutheria; Primates; Catarrhini; Hominidae; Sucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; 84 a Conservative /note="human" 1..345 /organism="Homo sapiens" Location/Qualifiers /clone="61440" 89 c 347 bp Score 14; DB 73; Pred. No. 3.47e-01; 0; Mismatches 6 RNA Ω FLP1st 112 t DB 73; Length 345; EST Ношо. 16-SEP-1994 **;** Gaps 0

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May 14 13:59

RESULT Ş 밁 ORIGIN BASE COUNT FEATURES COMMENT May 14 13:59 Query Match 53.8%; Best Local Similarity 60.0%; Matches D60505; 27-AUG-1995 (Rel. 45, Created) Fujiwara T., Hirano H., Katagiri T., Kawai A., Kuga Y., Nagata M., Okuno S., Ozaki K., Shimizu F., Shimada Y., Shinomiya H., Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Theria; Eutheria; Primates; Haplorhini; Catarrhini; source source Kawauchi-cho Tokushima, Submitted (30-May-1995) to DDBJ by: Tsutomu Fujiwara Otsuka GEN Research Institute Otsuka Pharmaceutical Co.,Ltd 463-10 kagasuno Unpublished. Maekawa H., Shin S., Nakamura Y.;
*Unpublished(101)"; Takaichi A., 1 - 369Homo sapiens (human similar to none (May 29, 1995). EST (expressed sequence tag); Human fetal brain; Human fetal brain cDNA 3'-end GEN-113E01. HS113E01A standard; RNA; EST; rax . 34 0886-37-1035 Cloning method: total mRNA was oligo-(dT) primed and directionally cloned 5' -> 3' into the HindIII -> NotI sites of the lafmid BA NCBI gi: Genexpress_sequence_idt: y1c-30g12. Genexpress_library_idt: C; Normalization_method: Bento Soares, Stretch removed: nothing cDNA sequence colinear to mRNA Primer: M13_reverse Sequencing_method: single read, vector; 18; 103 Takeda S., Watanabe T., Takahashi E.i., Hirai Y., Conservative Ø 706035 /isolate="muscular atrophy patient" 88 c 83 g 75 t 1 /clone_lib="normalized infant brain cDNA from Psychiatry Dept. Columbia University USA" /clone_lib="Clontech human fetal brain polyA+ mRNA (#6535) /organism="Homo sapiens" /sequenced_mol="cDNA to mRNA" /tissue_type="total brain"
/dev_stage="3 months old" Location/Qualifiers /sex="female" Location/Qualifiers /organism="Homo sapiens" Last updated, Version 1) Tokushima 771-01 Japan Phone: 0886-65-2888 Score 14; DB 27; Pred. No. 3.47e-01 0; 83 g 369 Mismatches ₽. FLP1st DB 27; full automatic; P.N.A.S. 91:9228-9232(1994); Length 350; 1 others Indels Mammalia; Hominidae. **;** B.Soares, Gaps 0

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Sequence 369 BP; 154 A; 57 C; 59 G; 90 T; 9 other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
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                                                                                    yh58f05.s1 Homo sapiens cDNA clone 133953 3'. R28016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          constructed by Bento Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vector. Library went through one round of normalization. Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I and cloned into the Pac I and Eco RI sites of the modified pT7T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         strand cDNA was primed with a Pac I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SP:TOA2_YEAST P32774 TRANSCRIPTION INITIATION FACTOR IIA SMALL
                       human clone=133953 library=Soares placenta Nb2HP vector=pT7T3D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stops: 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liver and spleen from a 20 week-post conception male fetus. 1st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human clone=129268 library=Soares fetal liver spleen 1NFLS
(Pharmacia) with a modified polylinker host=DH10B (ampicillin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ampicillin resistant) primer=M13RP1 Rsite1=Pac I Rsite2=Eco RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="human"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="129268"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                          418 bp
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                                                                                                                                                                                                                                                                                                                                                                                                   Score 14; DB 36;
Pred. No. 3.47e-01;
                                                                                                                                                                                                                                                                                                                                                                              <u>.</u>
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                                                                                                                                               ERNA
                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 others
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                                                                                                                                               25-APR-1995
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                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                   TOCUS
                                                                                                                                                                                                                                                                                                                                                                                 RESULT
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                                                                                                                                                                                                                                       SOURCE
                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 53.8%;
Best Local Similarity 60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 gaagttcctattcNNNNNNngtataggaa 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                      R01221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18;
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COMMENT

JOURNAL

Unpublished (1995)

Contact: Wilson RK

314 286 1800

REFERENCE

ORGANISM

Homo sapiens

Eutheria; Primates;

(bases 1 to 390)

AUTHORS

May 14 13:59 resistant) primer=Promega -21m13 Rsite1=Not I Rsite2=Eco RI Female

¥

cDNA was ligated to Eco RI adaptors (Pharmacia), vector. Library went through one round of normalization. Library with a Not I - oligo(dT) primer (5')constructed by Bento Soares and M.Fatima Bonaldo. I and cloned into the Not I and Eco RI sites of the modified pT7T3 digested with Not

Eutheria; Primates; Catarrhini; Hominidae; Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; Homo.

(bases 1 to 418)

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and

The WashU-Merck EST Project

Washington University School of Medicine WashU-Merck EST Project High quality sequence stops: 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Contact: Wilson RK Source: IMAGE Consortium, LLNL Email: est@watson.wustl.edu Fax: 314 286 1810 This clone is available royalty-free through LLNL; contact the 314 286 1800 Consortium (info@image.llnl.gov) for further information.

NCBI gi: 784151 1..418 Location/Qualifiers

/note="human" /organism="Homo sapiens" /clone="133953"

60 ი 85 g 137 t 4 others

DB 41; Length 418;

Gaps

0

167 gaagttettattgtacatgtagcatgggaa 196 Conservative Score 14; DB 41; Pred. No. 3.47e-01 0; Mismatches Indels <u>.</u>

ORIGIN

Query Match 53.8%; Best Local Similarity 62.5%;

15;

Conservative

BASE COUNT

114 a

73 c

FEATURES

NCBI gi:

763854

source

KEYWORDS DEFINITION RESULT

23

ACCESSION 2002 ႕

29

= =

38

R28016

ye81a01.s1 Homo sapiens cDNA clone 124104 3'. R01221 vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=-21ml3 Rsite1=Pac I Rsite2=Eco RI human clone=124104 library=Soares fetal liver spleen Library went through one round of normalization. Library 421 bp BRNA 31-MAR-1995

딿

SOURCE Ş 망 COMMENT KEYWORDS **FOCUS** RESULT ORIGIN BASE COUNT FEATURES REFERENCE ACCESSION DEFINITION Matches Best Local Similarity Query Match JOURNAL AUTHORS ORGANISM ORGANISM source 255 ttnctattcattctgtagtattgga 279 5 ttcctattcNNNNNNngtatagga 29 40 yd35c09.r1 Homo sapiens cDNA clone 110224 5' similar to gb|L13707|HUM5CALUE Human scRNA molecule, transcribed from Alu (rRNA); gb:J04970 CARBOXYPEPTIDASE M PRECURSOR (HUMAN);contains Alu Homo sapiens Homo sapiens repetitive element;. T71405 NCBI gi: Tel: Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Contact: Wilson RK WashU-Merck EST Project Unpublished (1995) Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Holman, M., Hultman, M., Hillier, L., Clark, N., Dubuque, T., Eutheria; Primates; Eucaryotae; Metazoa; constructed by Bento vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B human clone=110224 library=Soares fetal liver spleen INFLS High quality sequence stops: 361 Email: est@watson.wustl.edu The WashU-Merck EST Project Eutheria; Primates; Catarrhini; Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia; constructed by Bento Soares and M.Fatima Bonaldo. vector. Library went through one round of normalization. cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac strand cDNA was primed with a Pac I - oligo(dT) primer [5' IMAGE Consortium (info@image.llnl.gov) for further information. This clone is available royalty-free through LLNL; contact the Source: IMAGE Consortium, LLNL I and cloned into the Pac I and Eco RI sites of the modified pT7T3 Liver and spleen from a 20 week-post conception male fetus. 1st (ampicillin resistant) primer=M13RP1 Rsite1=Pac I Rsite2=Eco RI 15; (bases 1 to 421) 129 314 286 1810 314 286 1800 Conservative þ 750957 /note="human" /clone="124104" /organism="Homo sapiens" Location/Qualifiers 1..421 53.8%; 60.0%; 72 c Catarrhini; Chordata; Soares and M.Fatima Bonaldo Pred. No. 3.47e-01 Score 14; <u>.</u> 74 g Kucaba, T., Le, M., Lennon, G., Marra, M., Mismatches 142 t Vertebrata; DB 34; Length 421; Hominidae; Hominidae; Elliston, K., Hawkins, M., 10; 4 others Indels Нопю. Ношо. Gnathostomata; Mammalia; MO 63108 15-MAR-1995 <u>.</u>. Gaps Library <u>.</u>

> May 14 13:59 **FLP**.rst

> > 36

Ş 밁 COMMENT KEYWORDS ACCESSION DEFINITION rocas ORIGIN BASE COUNT FEATURES REFERENCE Query Match 53.8%; Best Local Similarity 62.5%; AUTHORS Matches JOURNAL source 145 attctttatttggtattggaactt 168 10 attcNNNNNNngtataggaactt 33 41 yp24g12.s1 Homo sapiens cDNA clone 188422 3' H44838 Tel: Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Other_ESTs: yd35c09.s1 Unpublished (1995) Holman, M., Hultman, M., Kucaba, T., Le Parsons, J., Rifkin, L., Rohlfing, T., Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., NCBI gi: 685926 This clone is available royalty-free through LLNL; contact the Source: IMAGE Consortium, LLNL High qality sequence stops: 327 WashU-Merck EST Project Contact: Wilson RK The WashU-Merck EST Project Wilson, R. double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), resistant) primer=Promega -21ml3 Rsite1=Not I Rsite2=Eco RI Adult Email: est@watson.wustl.edu Fax: 314 286 1810 Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and human clone=188422 library=Soares breast 3NbHBst vector=pT7T3D IMAGE Consortium (info@image.llnl.gov) for further information. numan. 1st strand cDNA was primed with a Not I - oligo(dT) primer (Pharmacia) with a modified polylinker host=DH10B (ampicillin 15; (bases 1 to 450) 111 314 286 1800 Conservative ຸໝ /organism="Homo sapiens" /clone="110224" /note="human" Location/Qualifiers 93 c Pred. No. 3.47e-01; Score 14; 110 g <u>,</u> Kucaba, T., Le, M., Lennon, G., Marra, M., Mismatches 133 t DB 81; Length 450; Soares, M., Tan, F., 9; Indels 3 others <u>.</u> Gaps <u>.</u>

digested with Not I and cloned into the Not I and Eco RI sites of of normalization to a Cot = 20. Library constructed by Bento Soares modified pT7T3 vector (Pharmacia). Library went through one round and M.Fatima Bonaldo.

REFERENCE AUTHORS ORGANISM Homo sapiens Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Choanata; Tetrapoda; Amniota; Hammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis, E., Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; (bases 1 to 468) Waterston, R., Williamson, A.,

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JOURNAL

Unpublished (1995)

The WashU-Merck EST Project

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38

Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

NCBI gi: 653465

FEATURES Location/Qualifiers

1..471
source 1..471
forganism="Homo sapiens"

/clone="72436"
/note="human"
BASE COUNT 143 a 81 c 95 g 150 t 2 others
ORIGIN

SOURCE KEYWORDS DEFINITION POCAR RESULT ACCESSION 3 representing the following areas of the brain: frontal, parietal, temporal and occipital cortex from the left and right hemispheres, vector=pT7T3D (Pharmacia) with a modified polylinker host=DH10B (ampicillin resistant) primer=M13Rev Rsite1=Not I Rsite2=Eco RI 55-year old male. 1st strand cDNA was primed with a Not I -EST. yo09d08.rl Homo sapiens cDNA clone 177423 5'. H42585 through one round of normalization to a Cot = 53. Library Homo sapiens clone=177423 library=Soares adult brain N2b5HB55Y H42585 constructed by Bento Soares and M.Fatima Bonaldo. The adult brain oligo(dT) primer [5' aortic aneurysm. RNA was prepared from a pool of tissues hours after death which occurred in consequence of a ruptured RNA was provided by Dr. Donald H. Gilden. Tissue was acquired 17-18 RI sites of a modified pT7T3 vector (Pharmacia). Library went double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco 473 bp **BRNA** 31-JUL-1995

Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata;
Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes;
Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria;
Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 473)
AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Parevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and

ORGANISM

Homo sapiens

midbrain, pons and medulla.

subcortical white matter, basal ganglia, thalamus, cerebellum,

Wilson, R.

TITLE The WashU-Merck EST Project
JOURNAL Unpublished (1995)

COMMENT Contact: Wilson RK
WashU-Merck EST Project
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800

΄.

RESULT Ş 맑 **FOCUS** FEATURES REFERENCE SOURCE KEYWORDS ACCESSION DEFINITION BASE COUNT Query Match 53.8%; Best Local Similarity 60.7%; ORGANISM Matches JOURNAL AUTHORS source 136 gttcttattcatatatttttataggcac 163 4 gttcctattcNNNNNNNgtataggaac 31 44 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Homo sapiens cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTTT3EST. yi99c10.rl Homo sapiens cDNA clone 147378 5'. H01413 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. High quality sequence stops: 169 Fax: 314 286 1810
Email: est@watson.wustl.edu Unpublished (1995) constructed by Bento Soares and M.Fatima Bonaldo. vector. Library went through one round of normalization. Library obtained at birth (full term). 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' H01413 NCBI gi: 918637 Source: IMAGE Consortium, LLNL 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Washington University School of Medicine WashU-Merck EST Project Contact: Wilson RK The WashU-Merck EST Project Eutheria; Archonta; Primates; Catarrhini; Hominidae; Homo. Sarcopterygii; Choanata; Tetrapoda; Amniota; Mammalia; Theria; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Eukaryotae; Metazoa; Eumetazoa; Bilateria; Coelomata; resistant) primer=M13RP1 Rsite1=Not I Rsite2=Eco RI Female placenta human clone=147378 library=Soares placenta Nb2HP vector=pT7T3D This clone is available royalty-free through LLNL; contact the High qality sequence stops: 339 Email: est@watson.wustl.edu Fax: 314 286 1810 Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and (Pharmacia) with a modified polylinker host=DH10B (ampicillin IMAGE Consortium (info@image.llnl.gov) for further information. (bases 1 to 476) 119 314 286 1800 Conservative /organism="Homo sapiens" /clone="177423" 1..473 Location/Qualifiers 79 c 476 bp Score 14; DB 16; Pred. No. 3.47e-01; Mismatches 98 g 162 t Length 473; 15 others Indels <u>.</u>. Gaps <u>,</u>

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င္မ 밁 FEATURES COMMENT REFERENCE SOURCE KEYWORDS ACCESSION DEFINITION RESULT ORIGIN BASE COUNT FEATURES Matches Query Match 53.8%; Best Local Similarity 65.4%; ORGANISM JOURNAL AUTHORS source source 386 gttcctatgcntattttttaatagga 411 31 gttcctatacNNNNNNNngaatagga 6 45 NCBI primer=-21m13 Rsite1=EcoRI Rsite2=XhoI Normal lung tissue from a 72
year old male. Cloned unidirectionally. Primer: Oligo dT. Average
insert size: 1.0 kb; Uni-ZAP XR Vector; 5' adaptor sequence:
5'-CAATTCGCACGAC-3'; 3' adaptor sequence: EST. yc13f05.s1 Homo sapiens cDNA clone 80577 3' similar to gb:D90150_rna1 GUANINE NUCLEOTIDE-BINDING PROTEIN G(Z), ALPHA Unpublished (1995) Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Tan,F., Trevaskis,E., Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Homo sapiens T59688 5'-CTCGAGTTTTTTTTTTTTTTTT-3'. vector=pBluescript SK- host=SOLR cells (kanamycin resistant) human clone=80577 library=Stratagene lung (#937210) SUBUNIT (HUMAN);. T59688 NCBI gi: 661525 Washington University School of Medicine WashU-Merck EST Project Contact: Wilson RK WashU-Merck EST Project Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R. [MAGE Consortium (info@image.llnl.gov) for further information. This clone is available royalty-free through LLNL; contact the Source: IMAGE Consortium, LLNL High qality sequence stops: 324 mail: est@watson.wustl.edu Fax: 314 286 1810 Eutheria; Primates; Catarrhini; Hominidae; Sucaryotae; Metazoa; Chordata; Vertebrata; 17; (bases 1 to 516) 137 **g**i: 314 286 1800 Forest Park Parkway, Box 8501, St. Conservative മ 864346 /note="human" /organism="Homo sapiens" /clone="147378" 1..476 /clone="80577" /organism="Homo sapiens" Location/Qualifiers ocation/Qualifiers 77 c 516 bp Score 14; DB 4; L Pred. No. 3.47e-01; **,**; 78 g Mismatches 177 t Length 476; 9 Louis, MO 63108 7 others Gnathostomata; Mammalia; Indels Ношо. 09-FEB-1995 <u>;</u> Gaps 0

BASE COUNT

148

/note="human"

110 c

102 g

151 t

5 others

May 14 13.59 FLP.rst 41

Search completed: Tue May 14 14:08:43 1996 Job time : 526 secs.

Set	Items	Description	
S1	1	AU=WAHL ? AND FLP	
S2	0	O'GORMAN S? AND FLP	49
S3	1	AU=O'GORMAN S? AND FLP	- 10,041
S4	0	AU="O'GORMAN S?" AND FLP	514
S5	1	FLP AND MICE	51
S6	9	(FRT OR FLP) AND TRANSGEN?	
?t6/3/1-	- 9		

6/3/1

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11994591 BIOSIS Number: 98594591

Genetic regulation of mec-3 gene expression implicated in the specification of the mechanosensory neuron cell types in Caenorhabditis elegans

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Development Growth & Differentiation 37 (5). 1995. 551-557.

Full Journal Title: Development Growth & Differentiation

ISSN: 0012-1592 Language: ENGLISH

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Inst. Biotechnol., Univ. Cambridge, Tennis Court Rd., Cambridge CB2 1QT, UK

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Dep. Botany and Plant Pathol., Purdue Univ., West Lafayette, IN 47907, USA

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Full Journal Title: Plant Journal

ISSN: 0960-7412 Language: ENGLISH

Print Number: Biological Abstracts Vol. 100 Iss. 008 Ref. 118307

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11521508 BIOSIS Number: 98121508

Site-specific Transgene Insertion: An Approach

Wigley P; Becker C; Beltrame J; Blake T; Crocker L; Harrison S; Lyons I;

McKenzie Z; Tearle R; Crawford R; Robins A

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Reproduction Fertility and Development 6 (5). 1994. 585-588.

Full Journal Title: Reproduction Fertility and Development

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11204786 BIOSIS Number: 97404786

A cell-autonomous, ubiquitous marker for the analysis of Drosophila genetic mosaics

Vincent J-P; Girdham C H; O'Farrell P H

Dep. Biochem. Biophysics, Univ. California at San Francisco, San Francisco, CA 94143-0048, USA

Developmental Biology 164 (1). 1994. 328-331.

Full Journal Title: Developmental Biology

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10922464 BIOSIS Number: 97122464

A new method for manipulating transgenes: Engineering heat tolerance in a complex, multicellular organism

Welte M A; Tetrault J M; Dellavalle R P; Lindquist S L

Howard Hughes Med. Inst., Univ. Chicago, 5841 South Maryland, MC 1028 Chicago, IL 60637, USA

Current Biology 3 (12). 1993. 842-853.

Full Journal Title: Current Biology

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Print Number: Biological Abstracts Vol. 097 Iss. 006 Ref. 072338

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FLP-MEDIATED RECOMBINATION IN THE VECTOR MOSQUITO AEDES-AEGYPTI MORRIS A C; SCHAUB T L; JAMES A A

DEP. MOL. BIOL. AND BIOCHEM., UNIV. CALIF., IRVINE, CALIF. 92717.

NUCLEIC ACIDS RES 19 (21). 1991. 5895-5900. CODEN: NARHA

Full Journal Title: Nucleic Acids Research

Language: ENGLISH

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11521508 BIOSIS Number: 98121508

Site-specific Transgene Insertion: An Approach

Wigley P; Becker C; Beltrame J; Blake T; Crocker L; Harrison S; Lyons I;

McKenzie Z; Tearle R; Crawford R; Robins A

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Reproduction Fertility and Development 6 (5). 1994. 585-588.

Full Journal Title: Reproduction Fertility and Development

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Methods to improve the production of transgenic animals are being developed. Conventional transgenesis, involving microinjection of DNA into fertilized eggs, has a number of limitations. These result from the inability to control both the site of transgene insertion and the number of gene copies inserted. The approach described seeks to overcome these problems and to allow single copy insertion of transgenes into a defined site in animal genomes. The method involves the use of embryonic stem cells, gene targeting and the FLP recombinase system.

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8208682 BIOSIS Number: 91129682

RECOMBINASE-MEDIATED GENE ACTIVATION AND SITE-SPECIFIC INTEGRATION IN MAMMALIAN CELLS

O'GORMAN S; FOX D T; WAHL G M

GENE EXPRESSION LAB., SALK INST. BIOL. STUDIES, LA JOLLA, CALIF. 92037. SCIENCE (WASHINGTON D C) 251 (4999). 1991. 1351-1355. CODEN: SCIEA Full Journal Title: SCIENCE (Washington D C)

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3(prm1)TC5(prm1)) adjacent to the top-strand cleavage point. The unlabeled substrate was a concatemer of S2 obtained by self-ligation (S2n). S2 also contained two mismatched spacer positions next to the top-strand cleavage site (5(prm1)AG3(prm1)/3(prm1)AA5(prm1)). Following strand swapping between S1 and S2, the spacers would be fully matched (5(prm1)AG3(prm1)/3(prm1)TC5(prm1) and 5(prm1)TT3(prm1)/3(prm1)AA5(prm1)). Strand cleavage and strand transfer products are designated CP and STP, respectively. S represents the substrate. The heterogeneity in strand transfer products results from the multiplicity of crossover points within S2n. For each reaction set with a complementing protein pair, the leftmost lane represents a reaction with the triad variant alone (at the same molar concentration as in the rightmost lane). The next three lanes represent reactions containing the triad variant and Flp(Y343F) in approximate molar ratios of 1:1, 1:1.5, and 1:2, respectively. Roughly 3 pmol of Flp(Y343F) was present per pmol of the Flp-binding element. Lane C represents an assay with no <u>Flp</u> or <u>Flp</u> variant added to the reaction. The <u>Flp</u> reaction shown in lane 2 contained S1 but not S2n. The product X likely arose by cleavage within S1 and subsequent phosphoryl transfer to the 5(prm1)-hydroxyl group of the unannealed top-strand oligodeoxynucleotide of S1 present in the reaction. The size of X, as measured against standard molecular size markers, fits this explanation. Note the presence of X in a reaction containing S1 alone (lane 2). WT, wild type.

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recombination by <u>Flp</u>, they do not allow us to distinguish among the three potential types of trans DNA cleavage, trans horizontal, trans vertical, and trans diagonal (6; Fig. 1A). Results obtained with half-site reactions tend to disfavor the trans-vertical mode, while distinction between the trans-horizontal and trans-diagonal modes is not possible. Our expressed preference for trans-diagonal cleavage (6) over trans-horizontal cleavage must be tempered by the possibility that half sites are likely to enjoy greater freedom of stacking interactions in solution over full sites (11; Fig. 1B). The critical question is: what is the cleavage mode in full-site recombination? The answer can be sought provided a tagged recombinase can be targeted to a specific binding arm within a full-site recombination complex.

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<u>Flp</u> assembles a functional active site from partial active sites during full-site recombination:

The apparent cis DNA cleavage by Int in full attB sites and Holliday junctions calls into question the pertinence of the active-site assembly by <u>Flp</u> during a half-site reaction to that during normal recombination. The design of full sites containing mismatched spacers has allowed us to address this issue directly. Complementation by step arrest variants of <u>Flp</u> to mediate strand cleavage in full sites supports the shared-active-site configuration during a normal recombination reaction. In a reaction carried out by a pair of <u>Flp</u> step arrest mutants, cleavage is executed by the protein partner harboring Tyr-343, thus virtually excluding the operation of an aberrant pathway during complementation.

Recently, mechanistic analyses of another Int family recombinase, Xer (responsible for stable chromosome partitioning in Escherichia coli), have become possible (5). Recombination in this system requires the combined action of two recombinases, XerC and XerD. The binding arms of the Xer target site encode specificities for each of the two protein monomers. The cleavage pattern observed with Xer is most easily explained by cis DNA cleavage, although one particular type of trans cleavage (trans vertical or partner trans; 6, 16) cannot be ruled out.

The (lambda) Int and Xer examples, contrasted with <u>Flp</u>, imply that Int family recombinases do not conform to the same rules in building their active sites. However, one suspects that, within the fully assembled active sites of these proteins, key catalytic residues must have the same relative spatial disposition. This would account for the fact that they follow the same chemistry of recombination. Global diversity and limited homology, which are the hallmarks of this family (3), would then make a strong case for mechanistic convergence (8, 16) among proteins that execute chemically identical reactions.

Which mode of trans cleavage does <u>Flp</u> follow?: While our results strongly support trans DNA cleavage during full-site

- FIG. 5. [GREY SCALE PLATE AVAILABLE] Complementation between Flp(Y343F) and double or triple triad mutants of Flp in full-site cleavage. The substrate was labeled at the 3(prm1) ends. The proteins used in the assays are indicated above the lanes. The substrate band (S) and the cleavage products (CL and CR) are labeled as in Fig. 3. A control reaction without Flp or Flp variants is shown in lane C.
- FIG. 6. [GREY SCALE PLATE AVAILABLE] Strand transfer in full sites by pairwise combinations of <u>Flp</u> step arrest mutants. The substrates used in the assay are schematically shown at the top. The labeled substrate S1 contained (sup32)P at the 3(prm1) end of the top strand and two spacer mismatches (5(prm1)TT3(prm1) and

3

The successful execution of strand exchange within a full site by a complementing pair of <u>Flp</u> variants fully corroborates the inference from half-site reactions that <u>Flp(Y343F)</u> (harboring an intact RHR triad) can facilitate not only strand cleavage but also strand joining by using a Tyr-343 residue and a 5(prm1)-hydroxyl group, respectively, donated in trans.

DISCUSSION

The partial-active-site-trans DNA cleavage model for <u>Flp</u> was first proposed to account for the pattern of DNA cleavage and strand transfer in half-site substrates by complementing

FIG. 3. [GREY SCALE PLATE AVAILABLE] Complementation between Flp(Y343F) and triad mutants of Flp in full-site substrates. The full site used in the assays is schematically represented at the top (Fig. 2). The parallel arrows represent the Flp-binding elements; the short vertical arrows indicate the points of strand cleavage by Flp. The two mismatched positions within the spacer adjacent to the cleavage sites are shown by the bubbles. DNA sequences unrelated to recombination are symbolized by the wavy lines. The asterisks stand for the (sup32)P label at the 3(prm1) ends. Products of cleavage from the top strand (left) and the bottom strand (right) are labeled CL and CR, respectively. The substrate band is designated S. The lane marked C is a reaction in which no Flp or Flp variant was added. WT, wild type.

FIG. 4. [GREY SCALE PLATE AVAILABLE] Identification of the protein partner responsible for strand cleavage during catalytic complementation. Strand cleavage assays were carried out by using the substrate used in reactions shown in Fig. 3. The radioactive label was placed at the 5(prm1) end of each strand (asterisks). The covalent DNA-protein complex resulting from strand cleavage by Flp (or a Flp variant) is called DPC; that derived from GST-Flp (or a GST-Flp variant) is called DPCG. The doublets corresponding to DPC or DPCG are most likely cleavage products derived from the top and bottom strands. The substrate DNA band is marked S. Flp and the Flp variants used in the reactions are indicated above the appropriate lanes. Lane C is a control reaction without added Flp or Flp variants. WT, wild type.

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pairs of catalytic <u>Flp</u> mutants (6, 7, 13). The validity of the model was then verified for the R recombinase from Z. rouxii in half-site strand transfer reactions (24). The simplicity and functional parsimony of the model led us to speculate that the rules of active-site assembly and of DNA cleavage are likely to extend beyond the yeast site-specific recombinases and encompass the entire Int family. Experiments with (lambda) Int and suicide attL, attB, or Holliday junction substrates have yielded rather paradoxical results (10, 16). While one set of results supports the <u>Flp</u> paradigm (10), the other set casts doubt on the generality of the model (16).

recombination could be kept hidden. However, difficulty in selectively binding a protein monomer to one of the two normal binding elements of the full-site substrate poses an impediment to the rigorous testing of this prediction. Nevertheless, the degree of cleavage reduction obtained upon the mixing of roughly equal amounts of <u>Flp</u> and <u>Flp(H305L, Y343F)</u> was consistent with inactivation of the wild-type partner in a double-mutant-wild-type protein pair (data not shown).

Strand transfer in bubbled full sites by pairwise combination of Flp(Y343F) and triad variants of Flp: According to the partial-active-site-trans-cleavage model, during complementation between a Flp triad mutant and Flp(Y343F), cleavage should occur on the scissile phosphodiester adjacent to the bound Flp(Y343F) (the cis configuration in Fig. 1A) and away from the triad mutant (the trans configuration in Fig. 1A) (6, Once the DNA 3(prm1)-phosphotyrosyl bond has been formed, Flp(Y343F) can facilitate the strand-joining reaction by using the 5(prm1)-hydroxyl group as the nucleophile (13, 17). In the bubbled full-site substrate, the spacer mismatch inhibits the joining reaction. However, if one used a pair of substrates (S1 and S2n in Fig. 6), each mismatched within its spacer but fully matched with the partner's spacer, strand joining within a substrate (parental mode) would be suppressed but that between partners (recombinant mode) would be encouraged. Even when the lack of a second pair of exchanges (as with a pair of complementing mutants) would tend to reverse this reaction, one might expect to trap some of the strand transfer product. With wild-type <u>Flp</u>, strand transfer products were formed from this pair of substrates (lane 3 in Fig. 6). The heterogeneity of strand transfer products results from the fact that one of the two DNA substrates (the nonradioactive one) was a concatemer of a single full site (S2) obtained by ligation. We resorted to this trick because, under our assay conditions, strand transfer efficiency was increased severalfold by increasing the length of at least one of the recombination partners. The size of the recombinant strand would depend on the site within S2n at which crossover occurred. In reactions containing Flp(Y343F) in combination with a triad single mutant or a triad double mutant, strand transfer was indeed detected (lanes 6 to 8, 10 to 12, 14 to 16, and 18 to 20 in Fig. 6). The low level of reaction compared with the wild type is not surprising. Since a single-strand transfer requires a matched pair of cleavage events within the two substrates (on the top strands or the bottom strands), only a reaction complex containing two appropriately positioned Flp(Y343F) and triad mutant monomers would be successful in completing an exchange event. Further, unlike, the wild-type reaction, the mutant pair reaction cannot execute the second pair of exchanges that yields the mature recombinant product. One would expect, therefore, that reversal of the first exchange (due to the absence of a second exchange) would be more pronounced in a reaction containing the complementing partners than in the wild-type reaction.

cleavage product corresponded in size to that obtained with GST-Flp (lane 9 in Fig. 4).

The pattern of DNA-protein adducts observed in the complementation reactions demonstrates that cleavage is carried out exclusively by the protein partner that harbors the active-site tyrosine. The simplest interpretation of the results is that it is indeed Tyr-343 that performs strand cleavage. The more complex scenario in which the active species is derived from the triad variant but is a surrogate nucleophile rather than Tyr-343 is not excluded. However, this possibility is strongly discounted by the fact that no complementation was obtained between Flp(Y343F) and a double variant altered at a triad position and Tyr-343 (data not shown).

The donor of Tyr-343 during catalytic complementation can be mutated at all triad positions: The shared-active-site model for Flp predicts that a Flp variant doubly or triply mutated in the RHR triad would be as competent as the single mutant in catalytic complementation with Flp(Y343F) provided their binding affinities for the target DNA do not differ significantly. This prediction has been verified in half-site recombination (7). We tested two triad double mutants and a triad triple mutant in combination with Flp(Y343F) in the cleavage assay with the bubbled full site (Fig. 5). Individually, neither the triad mutants nor Flp(Y343F) could effect strand cleavage (lanes 3, 4, 6, and 8 in Fig. 5). In contrast, each pair formed by mixing Flp(Y343F) and a triad mutant in roughly equimolar amounts exhibited approximately the same levels of complementation (lanes 5, 7, and 9 in Fig. 5). A second strong prediction of the partial-active-site model is that a triad mutant that also lacks Tyr-343 in combination with wild-type Flp will produce a catalytically inactive protein pair. This prediction could be directly tested in half-site reactions, since one could load the double mutant on a radioactively labeled half site and the wild-type protein on an unlabeled half site and then monitor

FIG. 2. Full-site substrates containing spacer mismatches. The sequences of the synthetic full sites used in the strand cleavage and strand transfer assays are shown. The <u>Flp</u>-binding elements are in boldface. Sequences flanking the <u>Flp</u> target site are represented by wavy lines. The positions of spacer mismatches (bubbles) are indicated. The experiments in which they were used are indicated by the corresponding figure numbers. S2n refers to a concatemer of S2 (8 to 10 monomeric units, on average). The spacer mismatches in S1 and S2 are such that strand swapping between the two substrates (following strand cleavage) would produce perfect complementarity.

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strand transfer only from the labeled substrate upon mixing of the prebound complexes (7). Thus, the background of wild-type

site is cleaved, the short spacer segment on the cleaved strand does not remain stably hydrogen bonded to its complementary sequence. Hence, it is effectively lost from the reaction center by diffusion. The 5(prm1)-hydroxyl group of the spacer on the noncleaved strand can then act as a phosphoryl acceptor to complete a half-site recombination event. Details of half-site reactions have been previously described (for example, see reference 22). Whereas two Flp monomers bound to a full site are restricted in their interactions by spacer connectivity, two half sites, each associated with a Flp monomer, are not subject to this constraint. They could potentially assume the configurations indicated. These correspond to variations of the trans interactions depicted in panel A.

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These results are consistent with the partial active-site model arrived at from half-site reactions (6). According to this model, a mutant pair can build an active site in which the RHR triad is contributed by $\underline{Flp}(Y343F)$ and Tyr-343 is contributed by the triad mutant. Therefore, strand cleavage becomes possible.

The nucleophile in the cleavage reaction by a pair of complementing <u>Flp</u> variants is Tyr-343: The partial-active-site model is based on the tacit assumption that strand cleavage is executed by the lone Tyr-343 present within a pair of the complementing protein monomers. The model would break down if, in the absence of Tyr-343, a substitute nucleophile in the form of a serine, threonine, cysteine, or another tyrosine could take up its function. We have ruled out the possibility of cis cleavage by a nucleophile other than Tyr-343 in complementation reactions with half sites (24). In the full-site context, activation of a surrogate nucleophile within Flp(Y343F) as a result of allosteric interactions among the protein monomers is not impossible. To test the surrogate nucleophile hypothesis, the assay was done with a bubbled full site labeled at the 5(prm1) end on both strands and a complementing pair of Flp variants made up of a normal-sized protein and a 30-kDa larger protein partner obtained as a fusion with GST. The protein-DNA adduct formed by Flp and the GST-Flp hybrid upon DNA cleavage can be distinguished by the difference in electrophoretic migration between them (lanes 2 and 3 in Fig. 4). Flp (Y343F) or GST-Flp(Y343F) did not yield the cleavage product, as expected (lanes 4 and 6 in Fig. 4). Flp(H305L) and GST-<u>Flp(H305L)</u> yielded low levels of the cleavage products with the expected mobilities (lanes 5 and 7 in Fig. 4). The low level of strand cleavage by these proteins was as predicted by the results shown in Fig. 3. However, in partnership with Flp (Y343F), they produced elevated levels of cleavage commensurate with catalytic complementation (lanes 8 and 9 in Fig. 4). When the complementing partners were GST-Flp(Y343F) and Flp(H305L), the size of the cleavage product matched that obtained from reactions with Flp (lane 8 in Fig. 4). When the reaction contained the reciprocal pair, Flp(Y343F) and GST-Flp(H305L), the

substrate (6, 17). However, attempts to obtain catalytic complementation between a triad mutant and Flp(Y343F) in full sites have not been successful. This is not surprising. In a recombination complex containing two monomers of each mutant oriented appropriately, a Holliday junction may be formed. Since the junction cannot be resolved into recombinants, the exchange reaction is reversed to restore the parental configuration. Demonstration of complementation therefore required the use of a suicide substrate in which the reaction intermediates could be readily trapped. We discovered that mismatches at certain positions within the strand exchange (spacer) region of a full site can strongly inhibit the strand-joining step of recombination, thus effectively transforming the sites harboring such mismatches into suicide substrates (unpublished data). For example, the substrate shown in Fig. 3 contains two adjacent mismatches each (bubbles) neighboring the cleavage points at the left and right ends of the spacer (Fig. 2). This substrate was cleaved efficiently by wild-type Flp. However, since strand joining was markedly slowed down (unpublished results), the cleavage product accumulated (lane 2 in Fig. 3). As expected, no cleavage was obtained with <u>Flp(Y343F)</u> (lane 3 in Fig. 3). <u>Flp</u> variants in which either of the two arginine residues from the RHR triad (Arg-191 and Arg-308) were changed failed to produce the cleavage product (lanes 4 and 8 in Fig. 3). It is known that Flp variants of the triad histidine can yield cleavage in a full site but are severely diminished in the ability to reseal strands (19). However, in a full site with the double bubble, cleavage by the histidine variants was significantly lowered relative to that obtained with wild-type Flp (compare lanes 6 and 2 in Fig. 3). It is possible that the absence of His-305, combined with the mismatched spacer configuration, perturbs the normal protein interactions that lead to catalysis. The histidine variants are also known to test as cleavage incompetent when provided with half-site substrates (23). When a triad arginine variant of Flp was mixed with Flp(Y343F), they complemented each other, as evidenced by the cleavage detected within the bubbled full site (lanes 5 and 9 in Fig. 3). Complementation was obtained when Flp (Y343F) was paired with the His-305 variant as well. Whereas cleavage with the His-305 variant alone was weak (lane 6 in Fig. 3), the complementing pair yielded much higher levels of cleavage (lane 7 in Fig. 3).

FIG. 1. Full-site and half-site substrates for <u>Flp</u> site-specific recombination. (A) Each full site contains two invertedly oriented <u>Flp</u>-binding elements (parallel arrows) bordering the strand exchange region (spacer). There is a one-to-one association between a binding element and a <u>Flp</u> monomer. Conceptually, a full site can be split into a left half site (L) and a right half site (R). The phosphodiesters involved in recombination between two full sites are indicated (p). The placement of a <u>Flp</u> monomer with respect to these phosphodiesters can be described as cis (a), trans horizontal (b), trans vertical (c), or trans diagonal (d). (B) A half site contains one <u>Flp</u>-binding element and one scissile phosphodiester. When the

mixture containing 250 mM Tris-HCl (pH 7.8), 4% sodium dodecyl sulfate, 40% glycerol, and 300 mM (beta)-mercaptoethanol. Suitable aliquots were heated at 95 deg C for 4 min and fractionated by electrophoresis in 8% polyacrylamide gels (12). The gels were rinsed in distilled water with gentle shaking, dried, and subjected to autoradiography.

General methods:

Restriction enzyme digestions, isolation of plasmid DNA, and other miscellaneous procedures were done as described by Maniatis et al. (14).

RESULTS

The normal <u>Flp</u> reaction uses two double-stranded DNA substrates, each containing a copy of the Flp recombination target sequence (Fig. 1A). These are referred to as full-site substrates. A recombination event between two full sites requires the cooperative action of four Flp monomers and involves the breakage and reformation of four phosphodiester bonds within DNA (two breakage-union steps within each substrate partner). The disposition of a target-bound Flp monomer with respect to the four scissile phosphodiester bonds can be described as cis, trans horizontal, trans vertical, or trans diagonal. Conceptually, a full site can be split into two half sites, a left half site and a right half site. Half-site substrates (Fig. 1B), originally designed for the (lambda) Int reaction (15) and subsequently adapted for the Flp reaction (2, 21, 22), have simplified the mechanistic analysis of site-specific recombination. A half site contains one Flp-binding element, one scissile phosphodiester, and one 5(prm1)-hydroxyl group that can act as a phosphoryl acceptor. Hence, it is capable of undergoing one strand cleavage and one strand-joining reaction, precisely half of the chemistry that a full site undergoes during a normal recombination event. However, while interactions between two Flp monomers within a full site are constrained by the continuous DNA segment between them (the strand exchange region or the spacer), half sites are not subject to such constraints. Hence, two half sites could potentially interact with each other in a variety of modes that may not be accessible to two full sites (Fig. 1B). A legitimate concern, then, is that direct extrapolations from half-site to full-site reactions may not always be valid. To overcome this impediment, the analyses described here were done with appropriately modified full-site substrates (Fig. 2).

Pairwise complementation between $\underline{Flp}(Y343F)$ and the RHR triad variants of \underline{Flp} during strand cleavage in full sites: It is known that a \underline{Flp} variant altered at one or more of the RHR triad positions in combination with a second variant

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lacking the active-site nucleophile, $\underline{Flp}(Y343F)$, can mediate a strand cleavage and a strand joining event within a half-site

heated to 65 deg C for 10 min, and cooled slowly to room temperature. The relevant features of these sites are described in Results and displayed in the figures. The complete sequences of the substrates are available upon request.

The 3(prm1) end of a deoxyoligonucleotide was labeled with (alpha)-(sup32)P-labeled cordycepin phosphate. Labeling at the 5(prm1) end was done by the T4 polynucleotide kinase reaction by using [(gamma)-(sup32)P]ATP as the phosphoryl donor. For some experiments, the 5(prm1) ends were phosphorylated with unlabeled ATP. The unreacted cordycepin phosphate or ATP was removed by spin dialysis on a G-25 column. Hybridization to the partner oligodeoxynucleotide was done in TE.

Strand cleavage assays:

Strand cleavage reactions were done under standard recombination conditions (6). Normally, 0.05 pmol of the 3(prm1) end-labeled substrate was reacted with approximately 0.5 pmol of Flp or a Flp variant (roughly 5 pmol of <u>Flp</u> per pmol of the binding element) in 30 (mu)l of the reaction mixture. Incubations were done at 30 deg C for 30 min. Reactions were stopped by immersing samples in a boiling water bath for 5 min. After addition of sodium dodecyl sulfate (final concentration, 0.1%) and proteinase K treatment (100 (mu)g per sample for 1 h at 37 deg C), samples were phenol-chloroform extracted and DNA was precipitated with ethanol. The DNA pellet was recovered by centrifugation, washed twice with 80% ethanol, and dried in vacuo. Strands were denatured in 95% formamide at 95 deg C, and samples were fractionated by electrophoresis in 10% denaturing polyacrylamide gels (acrylamide-bisacrylamide ratio, 19:1). Cleavage products were identified following autoradiography.

Strand transfer assays:

The synthetic full sites (approximately 45 to 50 bp long, carrying EcoRI and HindIII overhangs at the ends) were poor substrates in strand transfer. To increase the efficiency of the reaction, assays were done with the monomeric form of a radioactively labeled full site and the concatemeric form of the unlabeled full-site partner. The concatemer was prepared as follows. The full site phosphorylated at the 5(prm1) end on both strands was ligated at room temperature for 3 h under conditions that gave concatemers containing an average of 8 to 10 U of the monomer. The strand transfer reactions were done with the normal protocols described previously (6). The ratio of the labeled substrate to the monomeric equivalent of the unlabeled substrate was approximately 1:5. In these assays, approximately 6 to 8 pmol of <u>Flp</u> per pmol of the <u>Flp</u>-binding element was present in a reaction volume of 30 (mu)1. The samples were processed and fractionated as described for the strand cleavage assay.

Assay for formation of DNA-protein covalent adducts: Reactions were carried out under strand transfer conditions with a substrate labeled at the 5(prm1) ends on both strands. Reactions were quenched by addition of an equal volume of a stop

The catalytic strategies displayed by Flp and their mechanistic implications in recombination suggest that they may be universal to the Int family. One set of experiments with (lambda) Int using suicide attL substrates supports this notion. Catalytic complementation in pairwise combinations of the RHR triad mutants of Int with the active-site tyrosine mutant has been demonstrated (10). This result is strongly suggestive of trans DNA cleavage by Int. However, other results obtained by using suicide attB substrates and synthetic Holliday junctions are more parsimoniously explained in terms of cis DNA cleavage by Int (16).

The mechanistic dilemma posed by the Int results raises fundamental issues regarding the mechanism of Int family

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site-specific recombination. First, is the apparent cis-trans duality a basic feature of the reaction? Second, are there multiple modes of active-site assembly within this family? Finally, is the half-site reaction mechanistically distinct from the full-site reaction? We have devised an experimental design in which full sites carrying mismatches in the spacer region serve as substrates in complementation tests with step arrest Flp mutants. Our results fully support the shared active-site paradigm during full-site recombination. Furthermore, the mode of DNA cleavage is trans. We have found no evidence of cis-trans duality in <u>Flp</u> recombination.

MATERIALS AND METHODS

Purification of Flp:

Wild-type <u>Flp</u> and <u>Flp</u> variants were partially purified essentially as described by Prasad et al. (20). Strand cleavage and strand transfer assays were carried out with these preparations. Some reactions were done with 90 to 95% pure proteins obtained by an affinity purification protocol (18). Assays with affinity-pure proteins yielded the same results as those done with the less pure proteins. Fusion proteins composed of <u>Flp</u> (or a <u>Flp</u> variant) and glutathione S-transferase (GST) were purified in accordance with the procedure detailed by Yang and Jayaram (24). Protein concentrations were estimated by comparing densitometric scans of gel-fractionated aliquots stained with Coomassie brilliant blue to similar scans done with bovine serum albumin as the standard. These estimates were relatively crude and were only accurate within a factor of 2 or

Synthetic recombination sites: Oligodeoxynucleotides for construction of full sites were synthesized in an Applied Biosystems 380A DNA synthesizer by using phosphoramidite chemistry (4). Normally, 10 to 20 pmol of each of the two appropriate oligodeoxynucleotide pairs was mixed in TE (10 mM Tris-HCl [pH 7.8] at 23 deg C, 1 mM EDTA [pH 8.0]),

intermediate which, following branch migration, is resolved into recombinants by the second pair of cleavage-joining reactions. The Int family recombinases use an active-site tyrosine as the nucleophile to attack the scissile phosphodiester during the strand breakage step. In Flp, this tyrosine residue is Tyr-343 (9). The active-site tyrosine is one of the invariant tetrad residues of the Int family (1, 3). The other three invariant residues are two arginines and a histidine (the RHR triad; Arg-191, His-305, and Arg-308 in Flp). The strand cleavage reaction results in covalent attachment of the recombinase to the 3(prm1) phosphate of DNA and exposure of a 5(prm1)-hydroxyl group at the nick. Strand joining in the recombinant mode is then effected via nucleophilic attack, by the 5(prm1)-hydroxyl group from the nicked strand of one DNA substrate, on the 3(prm1)-phosphotyrosyl bond formed within the partner substrate.

The Int family recombinases exist in solution as monomers and bind to DNA as monomers. Four recombinase monomers must act cooperatively to accomplish one round of recombination. Two concerted break exchanges must be made at one end of the strand exchange region (spacer) to form the Holliday junction. The process then needs to be repeated at the other end of the spacer to resolve the junction into mature recombinants. How does an Int family recombinase coordinate the breakage-joining events within the two DNA substrates taking part in recombination? Does the recombinase have a built-in mechanism by which it avoids abortive partial reactions within an incompletely assembled reaction complex?

The active-site configuration of two Int family members, Flp and the Zygosaccharomyces rouxii recombinase R, inferred from recombination reactions containing half-site substrates and step arrest mutants of the recombinases suggests potential solutions to the problems addressed above (6, 7, 13, 17, 24). A monomer of Flp or R harbors a partial active site; a complete active site is assembled by contribution of residues from more than one recombinase monomer. In the shared active site, three of the invariant Int family residues, the RHR triad (Arg-191, His-305, and Arg-308 in Flp; Arg-207, His-317, and Arg-320 in R), are derived from one monomer; the active-site tyrosine (Tyr-343 in Flp and Tyr-358 in R) is provided by a second monomer (6, 17). Assembly of a functional active site from partial active sites neatly accommodates the observation that in reactions with half sites, an Flp or an R monomer does not cleave the substrate to which it is bound but rather cleaves the substrate bound by a second recombinase monomer (trans DNA cleavage; 6). The partial active site, together with the trans mode of DNA cleavage, suggests possible mechanisms for postponing the chemistry of recombination until the complex is fully organized, for simultaneously assembling two active sites for coordinated strand cleavages, and for coupling the cleavage reaction with the conformational switch required for strand joining between partner substrates.

Title: Active-Site Assembly and Mode of DNA Cleavage by Flp

Recombinase during Full-Site Recombination

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Abstract: A combination of half-site substrates and step

arrest mutants of Flp, a site-specific recombinase of the integrase family, had earlier revealed the following features of the half-site recombination reaction. (i) The Flp active site is assembled by sharing of catalytic residues from at least two monomers of the protein. (ii) A Flp monomer does not cleave the half site to which it is bound (DNA cleavage in cis); rather, it cleaves a half site bound by a second Flp monomer (DNA cleavage in trans). For the (lambda) integrase (Int protein), the prototype member of the Int family, catalytic complementation between two active-site mutants has been observed in reactions with a suicide attL substrate. By analogy with <a>Flp, this observation is strongly suggestive of a shared active site and of trans DNA cleavage. However, reactions with linear suicide attB substrates and synthetic Holliday junctions are more compatible with cis than with trans DNA cleavage. These Int results either argue against a common mode of active-site assembly within the Int family or challenge the validity of Flp half sites as mimics of the normal full-site substrates. We devised a strategy to assay catalytic complementation between Flp monomers in full sites. We found that the full-site reaction follows the shared active-site paradigm and the trans mode of DNA cleavage. These results suggest that within the

Int family, a unitary chemical mechanism of recombination is achieved by more than one mode of

physical interaction among the recombinase monomers.

Text:

The <u>Flp</u> protein of Saccharomyces cerevisiae is a conservative, site-specific DNA recombinase that belongs to the Int ((lambda) integrase) family of recombinases (1, 3). Members of this family execute recombination in two sequential steps. The first pair of strand cleavage-joining reactions produces a Holliday

172190 -----

Definition Yeast (S.cerevisiae) 2 micron circle plasmid, complete genome

GenBank Name: YSCPLASM, Accession: J01347

NCBI Seq ID: 172190

Organism Saccharomyces cerevisiae

Comment [8] sites; mRNA CAP sites and poly-adenylation sites. [9] sites; FLP binding.

[7] sites; FLP cleavage.

[11] sites; FLP-mediated recombination crossover site. Draft entry and clean copy sequence for [5] kindly provided by J.Senecoff, 24-JAN-1986.

Yeast 2 micron plasmid contains two 599 bp inverted repeats separated by a large unique (UL) and a small unique (US) region. During recombination the UL and US regions invert producing two sequence forms that differ in the orientation of one unique region relative to the other. The A form is presented below. FLP is the only 2-micron circleencoded protein needed for specific site recombination between the IRs of 2-micron circle. The minimal size of the recombination site required for efficient FLP recombinase-catalyzed recombination in vitro is no more than 28 bp, which includes parts of two 13 bp inverted repeats (positions 690-702 and 711-723) and all of an 8 bp spacer (703-710) [5]. The FLP recombinase cleaves the DNA at the boundaries of the spacer and becomes covalently linked to the spacer DNA [5],[9]. The efficiency of the recombination is reduced if the spacer in a recombinant site is increased or decreased by 1 bp, while the spacer in the second site is unaltered [5]. Recombination between two sites with identical 1-base pair additions or deletions is relatively unaffected, suggesting that pairing of sequences in the spacer regions is important in FLP-promoted recombination events [5]. The sequence asymmetry utilized by the recombinase to determine the orientation of the site is located uniquely within the spacer region. Another 13 bp direct repeat, is found at positions 676-688 [5]. FLP-mediated recombination involving two FLP sites that are inverted with respect to each other results in inversion of the DNA sequences between the sites [4]. If the participating recombination sites are in direct orientation, FLP promotes only the excision of the intervening DNA sequences [4]. The Rep 1 and Rep proteins are involved plasmid partitioning and protein stability.

A start codon in phase with the Rep1 coding region is located at positions 1966-1964. Two CAP sites for Rep1 mRNA are located beyond the 'atg' codon (position 2008) at positions 2004 and 2005. Complete source information:

Yeast (S. cerevisiae, strain A364A D5) DNA, clones pJDB71 [1], p82-6B [2], CV20 [3], pMMD2 [4], pGP20 [5], pJFS166 [10].

Updated

Jul 31, 1992

Coding region 172190: 5570..6318 172190: 1..523

Coding region 172190: c2008..887

Coding region 172190: 2271..2816

Coding region 172190: c5198..4308

Sequence 6318 nt, circular ds genomic

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1901 agtoccctt gtcgtctcga ttacacacct actttcatcg tacaccatag
1041 gttggaagtg ctgcataata cattgcttaa tacaagcaag cagtctctcg
2001 ccattcatat ttcagttatt ttccattaca gctgatgtca ttgtatatca
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2151 ttcgggaaaa agtagagcaa cgcgagttgc atttttaca ccataatgca
2201 tgattaactt cgagaaggga ttaaggctaa tttcactagt atgtttcaaa
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3751 aaaggtggat gggtaggtta tatagggata tagcacagag atatatagca

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4351 gttgctactc tcctttttt cgtgggaacc gctttagggc cctcagtgat
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4801 tatagttgct ttctattgtc taacagcttg ttattctgta gcatcaaatc
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5101 ggagcaatca tttcaataaa cagccgacat acatcccaga cgctataagc
5151 tgtacgtgct tttaccgtca gattcttggc tgtttcaatg tcgtccattt
5201 tggttttctt ttaccagtat tgttcgtttg ataatgtatt cttgcttatt
5251 acattataaa atctgtgcag atcacatgtc aaaacaactt tttatcacaa
5301 gatagtaccg caaaacgaac ctgcgggccg tctaaaaatt aaggaaaagc
5351 agcaaaggtg catttttaaa atatgaaatg aagataccgc agtaccaatt
5401 attttcgcag tacaaataat gcgcggccgg tgcatttttc gaaagaacgc
5451 gagacaaaca ggacaattaa agttagtttt tcgagttagc gtgtttgaat
5501 actgcaagat acaagataaa tagagtagtt gaaactagat atcaattgca
5551 cacaagateg gegetaagea tgecacaatt tggtatatta tgtaaaacac
5601 cacctaaggt gcttgttcgt cagtttgtgg aaaggtttga aagaccttca
5651 ggtgagaaaa tagcattatg tgctgctgaa ctaacctatt tatgttggat
5701 gattacacat aacggaacag caatcaagag agccacattc atgagctata
5751 atactatcat aagcaattcg ctgagtttcg atattgtcaa taaatcactc
5801 cagtttaaat acaagacgca aaaagcaaca attctggaag cctcattaaa
5851 gaaattgatt cctgcttggg aatttacaat tattccttac tatggacaaa
5001 aacatcaatc tgatatcact gatattgtaa gtagtttgca attacagttc
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5951 gaatcatcgg aagaagcaga taagggaaat agccacagta aaaaaatgct
6001 taaagcactt ctaagtgagg gtgaaagcat ctgggagatc actgagaaaa
6051 tactaaattc gtttgagtat acttcgagat ttacaaaaac aaaaacttta
6101 taccaattcc tcttcctagc tactttcatc aattgtggaa gattcagcga
6151 tattaagaac gttgatccga aatcatttaa attagtccaa aataagtatc
6201 tgggagtaat aatccagtgt ttagtgacag agacaaagac aagcgttagt
6251 aggcacatat acttctttag cgcaagggt aggatcgatc cacttgtata
6301 tttggatgaa tttttgag

486,489 PLEASE ENTER HOST PORT ID:x LOGINID: d184csl PASSWORD: TERMINAL (ENTER 1, 2, 3, 4, OR ?):2e P0001 U.S. Patent & Trademark Office 06 JUN 92 14:03:30 => set pagelength scroll SET COMMAND COMPLETED => s flp(5a)recombinas? 151 FLP 6 RECOMBINAS? 1 FLP(5A) RECOMBINAS? Ll => d 1. 4,997,757, Mar. 5, 1991, Process for detecting potential carcinogens; Robert H. Schiestl, 435/172.1, 6, 29, 172.3; 935/76, 78, 79, 84 [IMAGE AVAILABLE] => Alt-Z FOR HELP| VT102 | FDX | 2400 N81 | LOG CLOSED | PRINT OFF | ON-LINE d his (FILE 'USPAT' ENTERED AT 14:03:27 ON 06 JUN 92) SET PAGELENGTH SCROLL 1 S FLP(5A) RECOMBINAS? Ll L2 1 S L1 AND MAMMAL? FILE 'JPOABS' ENTERED AT 14:06:27 ON 06 JUN 92 L3 0 S L1 FILE 'USPAT' ENTERED AT 14:06:43 ON 06 JUN 92 => d 'L3' HAS NO ANSWERS Ø SEA FLP(5A)RECOMBINAS? $=> d_{11}$ 1. 4,997,757, Mar. 5, 1991, Process for detecting potential carcinogens; Robert H. Schiestl, 435/172.1, 6, 29, 172.3; 935/76, 78, 79, 84 [IMAGE AVAILABLE] edecyt ∵til <= FILE ' 'POABS' ENTERED AT 14:07:11 ON 06 JUN 92 JAPANESE PATENT ABSTRACTS * CURRENTLY, DATA IS LOADED THROUGH THE ABSTRACT PUBLICATION * * DATE OF AUGUST 30, 1991. * THE LATEST GROUPS RECEIVED ARE: C0862 E1105, M1150 & P1245. *

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21 FLP

Ø RECOMBINAS?

L4 0 FLP(5A)RECOMBINAS?

(Item 1 from file: 155) 2/3/1 08128396 92266396 *i*n trans by the active site tyrosine during Flp cleavage recombination: switching protein partners before exchanging strands. Chen JW; Lee J; Jayaram M Department of Microbiology, University of Texas, Austin 78712. Cell (UNITED STATES) May 15 1992, 69 (4) p647-58, ISSN 0092-8674 Journal Code: CQ4 Languages: ENGLISH Document type: JOURNAL ARTICLE 2/3/2 (Item 2 from file: 155) 08080444 92218444 Reactions between Malf- and full-FLP recombination target sites. A model system for analyzing early steps in FLP protein-mediated site-specific recombination. Qian XH; Inmay RB; Cox MM Department of Biochemistry, College of Agricultural and Life Sciences, University of Wisconsin, Madison 53706. J Biol Chem (UNITED STATES) 0021-9258 Journal Code: HIV Apr 15 1992, 267 (11) p7794-805, Contract/Grant No.: GM-32335; GM-14711 Languages: ENGLISH Document type: JOURNAL ARTICLE 2/3/3 (Item 3 from file: 155) 92051378 07913378 FLP-mediated regembination in the vector mosquito, Aedes aegypti. Morris AC; Schaub TL; James AA Department of Molecular Biology & Biochemistry, University of California, Irvine 92717/. Nucleic / Acids Res (ENGLAND) Nov 11 1991, 19 (21) p5895-900, ISSN 0305-1048 Journal Code: 08L Languages: ENGLISH Dogument type: JOURNAL ARTICLE 2/3/4 (Item 4 from fiڔe: 155) 07823652 91342652 Synapsis, strand scission, and strand exchange induced by the FLP recombinase: analysis with half-FRT sites. Amin A; Roca H; Luetke K; Sadowski PD Department of Medical Genetics, University of Toronto, Ontario, Canada. Mol Cell Biol Sep 1991, 11 (9) p4497-508, ISSN 0270-7306 Journal Code: NGY Languages: ENGLISH Document type: JOURNAL ARTICLE (Item 5 from file: 155) 07777737 91296737 Domain of a yeast site-specific recombinase (Flp) that recognizes its target site.

Chen JW; Evans BR; Yang SH; Teplow DB; Jayaram M
Department of Microbiology, University of Texas, Austin 78712.
Proc Natl Acad Sci U S A Jul 15 1991, 88 (14) p5944-8, ISSN 0027-8424
Journal Code: PV3

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/6 (Item 6 from file: 155)

07731454 91250454

Identification of the DNA-binding domain of the FLP recombinase.

Pan H; Clary D; Sadowski PD

Department of Medical Genetics, University of Toronto, Ontario, Canada.

J Biol Chem Jun 15 1991, 266 (17) p11347-54, ISSN 0021-9258

Journal Code: HIV Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/7 (Item 7 from file: 155)

07687992 91206992

Integration specificity of retrotransposons and retroviruses.

Sandmeyer SB; Hansen LJ; Chalker DL

Department of Microbiology and Molecular Genetics, College of Medicine, University of California, Irvine 92717.

Annu Rev Genet 1990, 24 p491-518, ISSN 0066-4197 Journal Code: 6DP Contract/Grant No.: GM33281

Languages: ENGLISH

Document type: JOURNAL ARTICLE; REVIEW; REVIEW, ACADEMIC

2/3/8 (Item 8 from file: 155)

07668658 91187658

A bacterial model system for chromosomal targeting.

Huang LC; Wood EA; Cox MM

Department of Biochemistry, College of Agricultural and Life Sciences, University of Wisconsin-Madison 53706.

Nucleic Acids Res Feb 11 1991, 19 (3) p443-8, ISSN 0305-1048 Journal Code: O&L

Contract/Grant No.: GM37835

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/9 (Item 9 from file: 155)

07645850 91164850

Recombinase-mediated gene activation and site-specific integration in mammalian cells.

O'Gorman S; Fox DT; Wahl GM

Gene Expression Laboratory, Salk Institute for Biological Studies, La Jolla, CA 92037.

Science Mar 15 1991, 251 (4999) p1351-5, ISSN 0036-8075

Journal Code: UJ7

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/10 (Item 10 from file: 155)

07643634 91162634

Tyr60 variants of Flp recombinase generate conformationally altered protein-DNA complexes. Differential activity in full-site and half-site recombinations.

Chen JW; Evans BR; Zheng L; Jayaram M

Department of Microbiology, University of Texas at Austin, Austin 78712.

J Mol Biol Mar 5 1991, 218 (1) p107-18, ISSN 0022-2836

Journal Code: J6V Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/11 (Item 11 from file: 155)

07554393 91073393

FLP protein of 2 mu circle plasmid of yeast induces multiple bends in the ${\sf FLP}$ recognition target site.

Schwartz CJ; Sadowski PD

Department of Medical Genetics, University of Toronto, Ontario, Canada.

J Mol Biol Nov 20 1990, 216 (2) p289-98, ISSN 0022-2836

Journal Code: JGV

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/12 (Item 12 from file: 155)

07553382 91072382

Protein-based asymmetry and protein-protein interactions in FLP recombinase-mediated site-specific recombination.

Qian XH; Inman RB; Cox MM

Program in Cell and Molecular Biology, College of Agricultural and Life Sciences, University of Wisconsin, Madison 53706.

J Biol Chem Dec 15 1990, 265 (35) p21779-88, ISSN 0021-9258

Journal Code: HIV

Contract/Grant No.: GM 37835; GM 14711

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/13 (Item 13 from file: 155)

07490349 91009349

Identification of the active site tyrosine of Flp recombinase. Possible relevance of its location to the mechanism of recombination [published erratum appears in J Biol Chem 1991 Apr 15;266(11):7312]

Evans BR; Chen JW; Parsons RL; Bauer TK; Teplow DB; Jayaram M Department of Molecular Biology, Research Institute of Scripps Clinic, La Jolla, California 92037.

J Biol Chem Oct 25 1990, 265 (30) p18504-10, ISSN 0021-9258 Journal Code: HIV

tames Code. MIV

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/14 (Item 14 from file: 155)

07410836 90317836

Synaptic intermediates promoted by the FLP recombinase.

Amin AA; Beatty LG; Sadowski PD

Department of Medical Genetics, University of Toronto, Ontario, Canada.

J Mol Biol Jul 5 1990, 214 (1) p55-72, ISSN 0022-2836

Journal Code: J6V

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/15 (Item 15 from file: 155)

07263960 90170960

Functional analysis of Arg-308 mutants of Flp recombinase. Possible role of Arg-308 in coupling substrate binding to catalysis.

Parsons RL: Evans BR: Zheng L: Jayaram M

Research Institute of Scripps Clinic, La Jolla, California 92037.

J Biol Chem Mar 15 1990, 265 (8) p4527-33, ISSN 0021-9258

Journal Code: HIV Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/16 (Item 16 from file: 155)

07229522 90136522

Use of site-specific recombination to regenerate selectable markers.

Cregg JM; Madden KR

Salk Institute Biotechnology/Industrial Associates, Inc., La Jolla, CA 92037.

Mol Gen Genet Oct 1989, 219 (1-2) p320-3, ISSN 0026-8925

Journal Code: NGP Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/17 (Item 17 from file: 155)

07190832 90097832

Characterization of Holliday structures in FLP protein-promoted site-specific recombination.

Meyer-Leon L; Inman RB; Cox MM

Program in Cellular and Molecular Biology, College of Agricultural and Life Sciences, University of Wisconsin-Madison 53706-1569.

Mol Cell Biol Jan 1990, 10 (1) p235-42, ISSN 0270-7306

Journal Code: NGY

Contract/Grant No.: GM37835; GM14711

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/18 (Item 18 from file: 155)

07123422 90030422

The FLP recombinase of yeast catalyzes site-specific recombination in the Drosophila genome.

Golic KG; Lindquist S

Howard Hughes Medical Institute, Department of Molecular Genetics and Cell Biology, University of Chicago, Illinois 60637.

Cell Nov 3 1989, 59 (3) p499-509, ISSN 0092-8674 Journal Code: CQ4

Contract/Grant No.: GM 25874

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/19 (Item 19 from file: 155)

07011744 89313744

Synthesis of an enzymatically active FLP recombinase in vitro: search for a DNA-binding domain.

Amin AA; Sadowski PD

Department of Medical Genetics, University of Toronto, Ontario, Canada.

Mol Cell Biol May 1989, 9 (5) p1987-95, ISSN 0270-7306

Journal Code: NGY Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/20 (Item 20 from file: 155)

07002130 89304130

FLP-FRT mediated intrachromosomal recombination on a tandemly duplicated YEp integrant at the ILV2 locus of chromosome XIII in Saccharomyces cerevisiae.

Rank GH; Arndt GM; Xiao W

Department of Biology, University of Saskatchewan, Saskatoon, Canada.

Curr Genet Feb 1989, 15 (2) p107-12, ISSN 0172-8083 Journal Code: CUG

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/21 (Item 21 from file: 155)

06876684 89178684

FLP recombinase of the 2 microns circle plasmid of Saccharomyces cerevisiae bends its DNA target. Isolation of FLP mutants defective in DNA bending.

Schwartz CJ; Sadowski FD

Department of Medical Genetics, University of Toronto, Ontario, Canada.

J Mol Biol Feb 20 1989, 205 (4) p647-58, ISSN 0022-2836

Journal Code: J6V Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/22 (Item 22 from file: 155)

06825220 89127220

Holliday intermediates and reaction by-products in FLP protein-promoted site-specific recombination.

Meyer-Leon L; Huang LC; Umlauf SW; Cox MM; Inman RB

Department of Biochemistry, College of Agriculture and Life Sciences, University of Wisconsin-Madison 53706-1569.

Mol Cell Biol Sep 1988, 8 (9) p3784-96, ISSN 0270-7306

Journal Code: NGY

Contract/Grant No.: GM37835; GM14711

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/23 (Item 23 from file: 155)

06823587 89125587

The mechanism of loading of the FLP recombinase onto its DNA target sequence.

Beatty LG; Sadowski PD

Department of Medical Genetics, University of Toronto, Ontario, Canada.

J Mol Biol Nov 20 1988, 204 (2) p283-94, ISSN 0022-2836

Journal Code: J6V

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/24 (Item 24 from file: 155)

06794920 89096920

Step-arrest mutants of FLP recombinase: implications for the catalytic mechanism of DNA recombination.

Parsons RL; Prasad FV; Harshey RM; Jayaram M

Department of Molecular Biology, Research Institute of Scripps Clinic, La Jolla, California 92037.

Mol Cell Biol Aug 1988, 8 (8) p3303-10, ISSN 0270-7306

Journal Code: NGY

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/25 (Item 25 from file: 155)

06761437 89063437

High frequency FLP-independent homologous DNA recombination of 2 mu plasmid in the yeast Saccharomyces cerevisiae.

Bruschi CV; Howe GA

Department of Microbiology and Immunology, School of Medicine, East Carolina University, Greenville, NC 27858-4354.

Curr Genet Sep 1988, 14 (3) p191-9, ISSN 0172-8083 Journal Code: CUG

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/26 (Item 26 from file: 155)

06740094 89042094

Holliday junctions in FLP recombination: resolution by step-arrest mutants of FLP protein.

Jayaram M; Crain KL; Parsons RL; Harshey RM

Department of Molecular Biology, Research Institute of Scripps Clinic, La Jolla, CA 92037.

Proc Natl Acad Sci U S A Nov 1988, 85 (21) p7902-6, ISSN 0027-8424 Journal Code: PV3

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/27 (Item 27 from file: 155)

06703077 89005077

The functional significance of DNA sequence structure in a site-specific genetic recombination reaction.

Umlauf SW; Cox MM

Department of Biochemistry, College of Agricultural and Life Sciences, University of Wisconsin-Madison 53706.

EMBO J Jun 1988, 7 (6) p1845-52, ISSN 0261-4189 Journal Code: EMB Contract/Grant No.: GM37835; AI00599; GM07215

Languages: ENGLISH

Document type: JOURNAL ARTICLE,

2/3/28 (Item 28 from file: 155)

06687975 88332975

DNA recognition by the FLP recombinase of the yeast 2 mu plasmid. A mutational analysis of the FLP binding site.

Senecoff JF; Rossmeissl PJ; Cox MM

Department of Biochemistry, College of Agricultural and Life Sciences, University of Wisconsin-Madison 53706.

J Mol Biol May 20 1988, 201 (2) p405-21, ISSN 0022-2836

Journal Code: J6V

Contract/Grant No.: GM37835; AI00599

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/29 (Item 29 from file: 155)

06643050 88288050

Nucleotide sequencing and expression of the fadL gene involved in long-chain fatty acid transport in Escherichia coli.

Said B; Ghosn CR; Vu L; Nunn WD

Department of Molecular Biology and Biochemistry, University of California, Irvine 92717.

Mol Microbiol May 1988, 2 (3) p363-70, ISSN 0950-382X

Journal Code: MOM

Contract/Grant No.: GM 22466-11

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/30 (Item 30 from file: 155)

06618001 88263001

FLP recombinase is an enzyme.

Gates CA; Cox MM

Department of Biochemistry, College of Agricultural and Life Sciences, University of Wisconsin-Madison 53706.

Proc Natl Acad Sci U S A Jul 1988, 85 (13) p4628-32, ISSN 0027-8424 Journal Code: PV3

Contract/Grant No.: GM37835; AI00599

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/31 (Item 31 from file: 155)

06567126 88212126

Mutations that improve the binding of yeast FLP recombinase to its substrate.

Lebreton B; Prasad FV; Jayaram M; Youderian P

Department of Biological Sciences, University of Southern California, Los Angeles 90089-1481.

Genetics Mar 1988, 118 (3) p393-400, ISSN 0016-6731 Journal Code: FNH

Contract/Grant No.: GM34982; GM35654

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/32 (Item 32 from file: 155)

06521666 88166666

Antagonistic controls regulate copy number of the yeast 2 mu plasmid. Murray JA; Scarpa M; Rossi N; Cesareni G

EMBL, Heidelberg, FRG.

EMBO J Dec 20 1987, 6 (13) p4205-12, ISSN 0261-4189 Journal Code: EMB

Languages: ENGLISH

2/3/33 (Item 33 from file: 155)

06506025 88151025

Autoregulation of 2 micron circle gene expression provides a model for maintenance of stable plasmid copy levels.

Som T; Armstrong KA; Volkert FC; Broach JR

Department of Molecular Biology, Princeton University, New Jersey 08544.

Cell Jan 15 1988, 52 (1) p27-37, ISSN 0092-8674 Journal Code: CQ4

Contract/Grant No.: GM34596

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/34 (Item 34 from file: 155)

06342913 87316913

Purification of the FLP site-specific recombinase by affinity chromatography and re-examination of basic properties of the system.

Meyer-Leon L; Gates CA; Attwood JM; Wood EA; Cox MM

Nucleic Acids Res Aug 25 1987, 15 (16) p6469-88, ISSN 0305-1048

Journal Code: O&L

Contract/Grant No.: GM32335; GM37835; AI00599; +

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/35 (Item 35 from file: 155)

06280212 87254212

Isolation of intermediates in the binding of the FLP recombinase of the yeast plasmid 2-micron circle to its target sequence.

Andrews BJ; Beatty LG; Sadowski PD

J Mol Biol Jan 20 1987, 193 (2) p345-58, ISSN 0022-2836

Journal Code: J6V Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/36 (Item 36 from file: 155)

06274060 87248060

Rapid localization and characterization of random mutations within the 2 micron circle site-specific recombinase: a general strategy for analysis of protein function [published erratum appears in Gene 1987;57(1):149]

Govind NS; Jayaram M

Gene 1987, 51 (1) p31-41, ISSN 0378-1119 Journal Code: FOP

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/37 (Item 37 from file: 155)

06210407 87184407

Site-specific recombination of the yeast plasmid two-micron circle: intermediates in the binding process.

Andrews BJ; Beatty LG; Sadowski PD

Basic Life Sci 1986, 40 p407-24, ISSN 0090-5542 Journal Code: 9K0

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/38 (Item 38 from file: 155)

06210406 87184406

Site-specific recombination promoted in vitro by the FLF protein of the yeast two-micron plasmid.

Senecoff JF; Bruckner RC; Meyer-Leon L; Gates CA; Wood E; Umlauf SW; Attwood JM; Cox MM

Basic Life Sci 1986, 40 p397-405, ISSN 0090-5542 Journal Code: 9K0 Contract/Grant No.: GM32335; 5-T32 GM07215; AI00599

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/39 (Item 39 from file: 155)

06210404 87184404

Survival strategies of the yeast plasmid two-micron circle.

Volkert FC; Wu LC; Fisher PA; Broach JR

Basic Life Sci 1986, 40 p375-96, ISSN 0090-5542 Journal Code: 9K0

Contract/Grant No.: GM34596; GM33132

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/40 (Item 40 from file: 155)

06201639 87175639

Mutations in the 2-microns circle site-specific recombinase that abolish recombination without affecting substrate recognition [published erratum appears in Froc Natl Acad Sci U S A 1988 Mar;85(5):1497]

Prasad PV; Young LJ; Jayaram M

Proc Natl Acad Sci U S A Apr 1987, 84 (8) p2189-93, ISSN 0027-8424 Journal Code: FV3

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/41 (Item 41 from file: 155)

06167165 87141165

Association of reciprocal exchange with gene conversion between the repeated segments of 2-micron circle.

Jayaram M

J Mol Biol Oct 5 1986, 191 (3) p341-54, ISSN 0022-2836

Journal Code: J6V

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/42 (Item 42 from file: 155)

06115790 87089790

Substrate recognition by the 2 micron circle site-specific recombinase: effect of mutations within the symmetry elements of the minimal substrate.

Prasad FV; Horensky D; Young LJ; Jayaram M

Mol Cell Biol Dec 1986, 6 (12) p4329-34, ISSN 0270-7306

Journal Code: NGY

Contract/Grant No.: GM 35654-01

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/43 (Item 43 from file: 155)

06115725 87089725

Mating type-like conversion promoted by the 2 micrograms circle

site-specific recombinase: implications for the double-strand-gap repair model.

Jayaram M

Mol Cell Biol Nov 1986, 6 (11) p3831-7, ISSN 0270-7306

Journal Code: NGY Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/44 (Item 44 from file: 155)

06115667 87089667

Identification of the crossover site during FLP-mediated recombination in the Saccharomyces cerevisiae plasmid 2 microns circle.

McLeod M; Craft S; Broach JR

Mol Cell Biol Oct 1986, 6 (10) p3357-67, ISSN 0270-7306

Journal Code: NGY Languages: ENGLISH

Document type: JOURNAL ARTICLE

' 2/3/45 (Item 45 from file: 155)

06090546 87064546

Interaction of the FLP recombinase of the Saccharomyces cerevisiae 2 micron plasmid with mutated target sequences.

Andrews BJ; McLeod M; Broach J; Sadowski FD

Mol Cell Biol Jul 1986, 6 (7) p2482-9, ISSN 0270-7306

Journal Code: NGY Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/46 (Item 46 from file: 155)

06009798 86310798

The FLP recombinase of the Saccharomyces cerevisiae 2 microns plasmid attaches covalently to DNA via a phosphotyrosyl linkage.

Gronostajski RM; Sadowski PD

Mol Cell Biol Nov 1985, 5 (11) p3274-9, ISSN 0270-7306

Journal Code: NGY

Languages: ENGLISH
Document type: JOURNAL ARTICLE

2/3/47 (Item 47 from file: 155)

06003314 86304314

Specific contacts between the FLP protein of the yeast 2-micron plasmid and its recombination site.

Bruckner RC: Cox MM

J Biol Chem Sep 5 1986, 261 (25) p11798-807, ISSN 0021-9258

Journal Code: HIV

Contract/Grant No.: GM32335; AI00599

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/48 (Item 48 from file: 155)

05983659 86284659

Chromatin organization of the Saccharomyces cerevisiae 2 microns plasmid depends on plasmid-encoded products.

Veit BE; Fangman WL

22

Mol Cell Biol Sep 1985, 5 (9) p2190-6, ISSN 0270-7306

Journal Code: NGY

Contract/Grant No.: GM18926

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/49 (Item 49 from file: 155)

05980709 86281709

FLP site-specific recombinase of yeast 2-micron plasmid. Topological features of the reaction.

Beatty LG; Babineau-Clary D; Hogrefe C; Sadowski PD

J Mol Biol Apr 20 1986, 188 (4) p529-44, ISSN 0022-2836

Journal Code: J6V Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/50 (Item 50 from file: 155)

05971102 86272102

Site-specific recombination promotes plasmid amplification in yeast.

Volkert FC; Broach JR

Cell Aug 15 1986, 46 (4) p541-50, ISSN 0092-8674 Journal Code: CQ4

Contract/Grant No.: GM-34596

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/51 (Item 51 from file: 155)

05958059 86259059

The minimal duplex DNA sequence required for site-specific recombination promoted by the FLP protein of yeast in vitro.

Proteau G; Sidenberg D; Sadowski P

Nucleic Acids Res Jun 25 1986, 14 (12) p4787-802, ISSN 0305-1048

Journal Code: O8L Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/52 (Item 52 from file: 155)

05931585 86232585

Sequence organization of the circular plasmid pKD1 from the yeast Kluyveromyces drosophilarum.

Chen XJ; Saliola M; Falcone C; Bianchi MM; Fukuhara H

Nucleic Acids Res Jun 11 1986, 14 (11) p4471-81, ISSN 0305-1048

Journal Code: O&L

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/53 (Item 53 from file: 155)

05923006 86224006

Directionality in FLP protein-promoted site-specific recombination is mediated by DNA-DNA pairing.

Senecoff JF; Cox MM

J Biol Chem Jun 5 1986, 261 (16) p7380-6, ISSN 0021-9258

Journal Code: HIV

Contract/Grant No.: GM32335; AI00599

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/54 (Item 54 from file: 155)

05919123 86220123

The integrase family of site-specific recombinases: regional similarities and global diversity.

Argos P; Landy A; Abremski K; Egan JB; Haggard-Ljungquist E; Hoess RH; Kahn ML; Kalionis B; Narayana SV; Pierson LS 3d; et al

EMBO J Feb 1986, 5 (2) p433-40, ISSN 0261-4189 Journal Code: EMB

Contract/Grant No.: AI 13544

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/55 (Item 55 from file: 155)

05810590 86111590

Site-specific recombinases: changing partners and doing the twist. Sadowski ${\sf P}$

J Bacteriol Feb 1986, 165 (2) p341-7, ISSN 0021-9193 Journal Code: HH3

Languages: ENGLISH

Document type: JOURNAL ARTICLE; REVIEW

2/3/56 (Item 56 from file: 155)

05741647 86042647

The FLP recombinase of the yeast 2-micron plasmid: characterization of its recombination site.

Senecoff JF; Bruckner RC; Cox MM

Proc Natl Acad Sci U S A Nov 1985, 82 (21) p7270-4, ISSN 0027-8424 Journal Code: PV3

Contract/Grant No.: GM32335

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/57 (Item 57 from file: 155)

05707309 86008309

The FLP protein of the 2-micron plasmid of yeast. Inter- and intramolecular reactions.

Gronostajski RM; Sadowski PD

J Biol Chem Oct 5 1985, 260 (22) p12328-35, ISSN 0021-9258 Journal Code: HIV

Lamburger CHOLTO

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/58 (Item 58 from file: 155)

05707308 86008308

Determination of DNA sequences essential for FLP-mediated recombination by a novel method.

Gronostajski RM; Sadowski PD

J Biol Chem Oct 5 1985, 260 (22) p12320-7, ISSN 0021-9258

Journal Code: HIV

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/59 (Item 59 from file: 155)

05707307 86008307

The FLP protein of the 2-micron plasmid of yeast. Purification of the protein from Escherichia coli cells expressing the cloned FLP gene.

Babineau D; Vetter D; Andrews BJ; Gronostajski RM; Proteau GA; Beatty LG; Sadowski PD

J Biol Chem Oct 5 1985, 260 (22) p12313-9, ISSN 0021-9258

Journal Code: HIV

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/60 (Item 60 from file: 155)

05560933 85176933

The FLP recombinase of the 2 micron circle DNA of yeast: interaction with its target sequences.

Andrews BJ; Proteau GA; Beatty LG; Sadowski PD

Cell Apr 1985, 40 (4) p795-803, ISSN 0092-8674 Journal Code: CQ4

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/61 (Item 1 from file: 5)

8906509 BIOSIS Number: 42131509

AN ORDERED DISASSEMBLY OF COMPLEXES OF FLP RECOMBINASE AND FRT SITES FOLLOWING RECOMBINATION

WAITE L L; COX M M

DEP. BIOCHEM., UNIV. WISCONSIN, MADISON, WIS. 53706.

KEYSTONE SYMPOSIUM ON MOLECULAR MECHANISMS IN DNA REPLICATION AND RECOMBINATION, TAOS, NEW MEXICO, USA, JANUARY 25-FEBRUARY 1, 1992. J CELL BIOCHEM SUPPL 0 (16 PART B). 1992. G7. CODEN: JCBSD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/62 (Item 2 from file: 5)

8906501 BIOSIS Number: 42131501

LIGATION ACTIVITY OF THE FLP RECOMBINASE

PAN G; SADOWSKI P D

DEP. MOLECULAR MED. GENETICS, UNIV. TORONTO, TORONTO, ONTARIO M5S 1A8, CAN.

KEYSTONE SYMPOSIUM ON MOLECULAR MECHANISMS IN DNA REPLICATION AND RECOMBINATION, TAOS, NEW MEXICO, USA, JANUARY 25-FEBRUARY 1, 1992. J CELL BIOCHEM SUPPL 0 (16 PART B). 1992. 65. CODEN: JCBSD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/63 (Item 3 from file: 5)

8906498 BIOSIS Number: 42131498

HALF-SITE RECOMBINATIONS MEDIATED BY FLP RECOMBINASE FROM SACCHAROMYCES-CEREVISIAE

SERRE M-C; LEI-ZHENG; JAYARAM M

DEP. MICROBIOL., UNIV. TEXAS AUSTIN, AUSTIN, TEX. 78746.

KEYSTONE SYMPOSIUM ON MOLECULAR MECHANISMS IN DNA REPLICATION AND RECOMBINATION, TAOS, NEW MEXICO, USA, JANUARY 25-FEBRUARY 1, 1992. J CELL BIOCHEM SUPPL 0 (16 PART B). 1992. 64. CODEN: JCBSD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/64 (Item 4 from file: 5) 8906492 BIOSIS Number: 42131492 FUNCTIONAL ANALYSES OF MUTANTS OF FLP AND R RECOMBINASE FROM YEAST CHEN J-W; LEE J; EVANS B; SERRE M-C; ARAKI H; OSHIMA Y; JAYARAM M DEP. MICROBIOL., UNIV. TEXAS AUSTIN, AUSTIN, TEX. 78712. KEYSTONE SYMPOSIUM ON MOLECULAR MECHANISMS IN DNA REPLICATION AND RECOMBINATION, TAOS, NEW MEXICO, USA, JANUARY 25-FEBRUARY 1, 1992. J CELL RIOCHEM SUPPL 0 (16 PART B). 1992. 62. CODEN: JCBSD Language: ENGLISH Document Type: CONFERENCE PAPER 2/3/65 (Item 5 from file: 5) 8197568 BIOSIS Number: 91118568 TYROSINE-60 VARIANTS OF FLP RECOMBINASE GENERATE CONFORMATIONALLY ALTERED PROTEIN DNA COMPLEXES DIFFERENTIAL ACTIVITY IN FULL-SITE AND HALF RECOMBINATIONS CHEN J-W; EVANS B R; ZHENG L; JAYARAM M DEP. MICRBOIOL., UNIV. TEXAS AUSTIN, AUSTIN, TEX. 78712, USA. J MOL BIOL 218 (1). 1991. 107-118. CODEN: JMOBA Full Journal Title: Journal of Molecular Biology Language: ENGLISH 2/3/66 (Item 6 from file: 5) 7103760 BIOSIS Number: 88026505 FLP-FRT MEDIATED INTRACHROMOSOMAL RECOMBINATION ON A TANDEMLY DEPLICATED YE-P INTEGRANT AT THE ILV2 LOCUS OF CHROMOSOME XIII IN SACCHAROMYCES-CEREVISIAE RANK G H; ARNDT G M; XIAO W DEP. BIOL., UNIV. SASKATCHEWAN, SASKATOON, SASKATCHEWAN, CANADA S7N 0W0. CURR GENET 15 (2). 1989. 107-112. CODEN: CUGED Full Journal Title: Current Genetics Language: ENGLISH 2/3/67 (Item 7 from file: 5) 7043154 BIOSIS Number: 87103675 FLP RECOMBINASE OF THE 2 MUM CIRCLE PLASMID OF SACCHAROMYCES-CELEVISIAE BENDS ITS DNA TARGET ISOLATION OF FLP MUTANTS DEFECTIVE IN DNA BEHDING SCHWARTZ C J E; SADOWSKI P D DEP. MED. GENETICS, UNIV. TORONTO, TORONTO, ONTARIO M5S 1A8, CAN. J MOL BIOL 205 (4). 1989. 647-658. CODEN: JMOBA Full Journal Title: Journal of Molecular Biology Language: ENGLISH 2/3/68 (Item 8 from file: 5) BIOSIS Number: 87004981 HIGH FREQUENCY FLF-INDEPENDENT HOMOLOGOUS DNA RECOMBINATION OF 2 MICRON PLASMID IN THE YEAST SACCHAROMYCES-CEREVISIAE BRUSCHI C V; HOWE G A DEP. MICROBIOL. IMMUNOL., SCH. MED., EAST CAROLINA UNIV., GREENVILLE, N.C. 27858-4354, U.S.A. CURR GENET 14 (3). 1988. 191-200. CODEN: CUGED Full Journal Title: Current Genetics

Language: ENGLISH

2/3/69 (Item 9 from file: 5)

6892306 BIOSIS Number: 37086685

THE FLP RECOMBINASE STEP-ARREST MUTANTS AND INTERMEDIATES IN RECOMBINATION

JAYARAM M; PARSONS R; EVANS B

RES. INST. SCRIPPS CLIN., LA JOLLA, CALIF. 92037.

SYMPOSIUM ON MOLECULAR MECHANISMS IN DNA REPLICATION AND RECOMB NATION HELD AT THE 18TH ANNUAL UCLA (UNIVERSITY OF CALIFORNIA-LOS ANGELE:) SYMPOSIA ON MOLECULAR AND CELLULAR BIOLOGY, STEAMBOAT SPRINGS, CO ORADO, USA, MARCH 27-APRIL 3, 1989. J CELL BIOCHEM SUPPL Ø (13 PART D). 989. 106. CODEN: JCBSD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/70 (Item 10 from file: 5)

6636107 BIOSIS Number: 86102658

AUTOREGULATION OF 2-MUM CIRCLE GENE EXPRESSION PROVIDES A MODEL FOR MAINTENANCE OF STABLE PLASMID COPY LEVELS

SOM T; ARMSTRONG K A; VOLKERT F C; BROACH J R

DEP. MOLECULAR BIOL., PRINCETON UNIV., PRINCETON, NEW JERSEY 08:144.

CELL 52 (1). 1988. 27-38. CODEN: CELLB

Full Journal Title: Cell

Language: ENGLISH

2/3/71 (Item 11 from file: 5)

6624830 BIOSIS Number: 86091381

THE INT FAMILY OF SITE-SPECIFIC RECOMBINASES SOME THOUGHTS ON A GENERAL REACTION MECHANISM

JAYARAM M

DEP. MOL. BIOL., RES. INST. SCRIPPS CLINIC, 10666 NORTH TORREY PINES ROAD, LA JOLLA, CALIF. 92037, USA.

J GENET 67 (1). 1988. 29-36. CODEN: JOGNA

Full Journal Title: Journal of Genetics

Language: ENGLISH

2/3/72 (Item 12 from file: 5)

6571174 BIOSIS Number: 86037725

FLP RECOMBINASE INDUCTION OF THE BREAKAGE-FUSION-BRIDGE CYCLE AND GENE CONVERSION IN SACCHAROMYCES-CEREVISIAE

RANK G H; XIAO W; KOLENOVSKY A; ARNDT G

DEP. BIOL., UNIV. SASK., SASKATOON, SASK., CAN. S7N OWO.

CURR GENET 13 (4). 1988. 273-282. CODEN: CUGED

Full Journal Title: Current Genetics

Language: ENGLISH

2/3/73 (Item 13 from file: 5)

6150196 BIOSIS Number: 35015717

PURIFICATION OF FLP RECOMBINASE USING SEQUENCE-SPECIFIC DNA AFF NITY CHROMATOGRAPHY

GATES C A; MEYER-LEON L; ATTWOOD J M; WOOD E A; COX M M

DEP. BIOCHEM., UNIV. WIS.-MADISON, MADISON, WIS. 53706, USA.

BURGESS, R. (ED.). UCLA (UNIVERSITY OF CALIFORNIA-LOS ANGELES) GYMPOSIA ON MOLECULAR AND CELLULAR BIOLOGY NEW SERIES, VOL. 68. PROTEIN PURIFICATION: MICRO TO MACRO; CETUS-UCLA SYMPOSIUM, FRISCO, COLORADO, USA, MARCH 29-APRIL 4, 1987. XVIII+510P. ALAN R. LISS, INC.: NEW YORK, NEW YORK, USA. ILLUS. ISBN 0-8451-2667-9. 0 (0). 1987. 197-206. CODEN: USMBD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/74 (Item 14 from file: 5)

5802738 FIOSIS Number: 83065045

SUBSTRATE RECOGNITION BY THE 2-MICROMETER CIRCLE SITE-SPECIFIC RECOMBINASE EFFECT OF MUTATIONS WITHIN THE SYMMETRY ELEMENTS OF THE MINIMAL SUBSTRATE

PRASAD F V; HORENSKY D; YOUNG L-J; JAYARAM M

DEP. MOL. BIOL., RES. INST. SCRIPPS CLIN., LA JOLLA, CALIF. 92037, USA.

MOL CELL BIOL 6 (12). 1986. 4329-4334. CODEN: MCERD

Full Journal Title: Molecular and Cellular Biology

Language: ENGLISH

2/3/75 (Item 15 from file: 5)

5761770 BIOSIS Number: 83024077

MATING TYPE-LIKE CONVERSION PROMOTED BY THE 2 MICROMETER CIRCLE SITE-SPECIFIC RECOMBINASE IMPLICATIONS FOR THE DOUBLE-STRAND-GAP REPAIR MODEL

JAYARAM M

DEP. MOLECULAR BIOLOGY, RESEARCH INST. SCRIPPS CLINIC, LA JOLLA, CALIFORNIA 92037.

MOL CELL BIOL 6 (11). 1986. 3831-3837. CODEN: MCEBD Full Journal Title: Molecular and Cellular Biology Language: ENGLISH

2/3/76 (Item 16 from file: 5)

5751545 BIOSIS Number: 83013852

ASSOCIATION OF RECIPROCAL EXCHANGE WITH GENE CONVERSION BETWEEN THE REPEATED SEGMENTS OF 2-MICROMETER CIRCLE

JAYARAM M

DEPARTMENT OF MOLECULAR BIOLOGY, RESEARCH INSTITUTE OF SCRIPPS CLINIC, 10666 NORTH TORREY PINES ROAD, LA JOLLA, CALIF. 92037, USA.

J MOL BIOL 191 (3). 1986. 341-354. CODEN: JMORA

Full Journal Title: Journal of Molecular Biology

Language: ENGLISH

2/3/77 (Item 17 from file: 5)

5696494 BIOSIS Number: 33091515

MECHANISMS OF ACTION OF THE FLP RECOMBINASE OF THE 2-MICRON PLASMID OF YEAST

SADOWSKI P D; BEATTY L G; CLARY D; OLLERHEAD S

DEP. MED. GENETICS, MED. SCIENCES BUILD., UNIV. TORONTO, TORONTO, CANADA M5S 1A8.

MCMACKEN, R. AND T. J. KELLY (ED.). UCLA (UNIVERSITY OF CALIFORNIA-LOS ANGELES) SYMPOSIA ON MOLECULAR AND CELLULAR BIOLOGY NEW SERIES, VOL. 47. DNA REPLICATION AND RECOMBINATION; PARK CITY, UTAH, USA, MARCH 16-23, 1986. XXVI+782P. ALAN R. LISS, INC.: NEW YORK, NEW YORK, USA. ILLUS. ISBN 0-8451-2646-6. 0 (0). 1987. 691-702. CODEN: USMBD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/78 (Item 18 from file: 5)

5504855 BIOSIS Number: 32027162

INTERACTION OF THE FLP RECOMBINASE OF THE 2-MICRON PLASMID WITH ITS TARGET SEQUENCE

SADOWSKI P D; ANDREWS B J; BEATTY L G; SIDENBERG D; PROTEAU G DEP. MED. GENETICS, UNIV. TORONTO, TORONTO M5S 1A8, CAN.

KLAR, A. AND J. N. STRATHERN (ED.). CURRENT COMMUNICATIONS IN MOLECULAR BIOLOGY: MECHANISMS OF YEAST RECOMBINATION; MEETING, COLD SPRING HARBOR, N.Y., USA. IX+193F. COLD SPRING HARBOR LABORATORY: COLD SPRING HARBOR, N.Y., USA. ILLUS. PAPER. ISBN 0-87969-195-6. 0 (0). 1986. 7-10. CODEN: 24607

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/79 (Item 19 from file: 5)

5426144 BIOSIS Number: 82070947

INTERACTION OF THE FLP RECOMBINASE OF THE SACCHAROMYCES-CEREVISIAE 2 MICROMETER PLASMID WITH MUTATED TARGET SEQUENCES

ANDREWS & J; MCLEOD M; BROACH J; SADOWSKI P D

DEP. OF MED. GENETICS, UNIV. OF TORONTO, TORONTO, ONTARIO M5S 1A8, CANADA.

MOL CELL BIOL 6 (7). 1986. 2482-2489. CODEN: MCEBD Full Journal Title: Molecular and Cellular Biology Language: ENGLISH

2/3/80 (Item 20 from file: 5) 5389362 BIOSIS Number: 82034165

FLP SITE-SPECIFIC RECOMBINASE OF YEAST 2-MICROMETER PLASMID TOPOLOGICAL FEATURES OF THE REACTION

BEATTY L G; BABINEAU-CLARY D; HOGREFE C; SADOWSKI P D
DEP. OF MED. GENETICS, UNIV. OF TORONTO, TORONTO M5S 1A8, CANADA.
J MOL BIOL 188 (4). 1986. 529-544. CODEN: JMOBA
Full Journal Title: Journal of Molecular Biology
Language: ENGLISH

2/3/81 (Item 21 from file: 5)

5265813 BIOSIS Number: 81033120

THE FLP RECOMBINASE OF THE SACCHAROMYCES-CEREVISIAE 2 MICROMETER PLASMID ATTACHES COVALENTLY TO DNA VIA A PHOSPHOTYROSYL LINKAGE

GRONOSTAJSKI R M; SADOWSKI P D

DEP. MED. GENET., UNIV. TORONTO, TORONTO, ONT. M5S1A8, CAN. MOL CELL BIOL 5 (11). 1985. 3274-3279. CODEN: MCEBD Full Journal Title: Molecular and Cellular Biology Language: ENGLISH

2/3/82 (Item 22 from file: 5) 5256098 BIOSIS Number: 81023405

THE FLP PROTEIN OF THE 2-MICRON PLASMID OF YEAST SACCHAROMYCES-CEREVISIAE PURIFICATION OF THE PROTEIN FROM ESCHERICHIA-COLI CELLS EXPRESSING THE CLONED FLP GENE

BABINEAU D; VETTER D; ANDREWS B J; GRONOSTAJSKI R M; PROTEAU G A; BEATTY L G; SADOWSKI P D

DEP. MED. GENETICS, UNIV. TORONTO, TORONTO, M5S 1A8, CANADA.

J BIOL CHEM 260 (22). 1985. 12313-12319. CODEN: JBCHA Full Journal Title: Journal of Biological Chemistry Language: ENGLISH

2/3/83 (Item 23 from file: 5) 5168213 BIOSIS Number: 31057528

THE FLP RECOMBINASE OF THE 2-MICRON PLASMID OF YEAST

SADOWSKI P D; ANDREWS B J; BABINEAU-CLARY D; BEATTY L; GRONOSTAJSKI R M; FROTEAU G; SIDENBERG D

DEP. MED. GENET., UNIV. TORONTO, TORONTO M5S 1A8, CANADA.

SYMPOSIUM ON MECHANISMS OF DNA REPLICATION AND RECOMBINATION HELD AT THE 15TH ANNUAL MEETING OF THE UCLA (UNIVERSITY OF CALIFORNIA-LOS ANGELES) SYMPOSIA ON MOLECULAR AND CELLULAR BIOLOGY, MAR. 16-23, 1986. J CELL BIOCHEM SUPPL 0 (10 PART B). 1986. 137. CODEN: JCBSD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/84 (Item 24 from file: 5) 4696890 BIOSIS Number: 29054205

INTERACTION OF THE FLP RECOMBINASE WITH SUBSTRATE 2-MICRON CIRCLE DNA ANDREWS & J; BEATTY L; SADOWSKI P D UNIV. TORONTO.

SYMPOSIUM ON YEAST CELL BIOLOGY HELD AT THE 14TH ANNUAL MEETING OF THE UCLA (UNIVERSITY OF CALIFORNIA - LOS ANGELES) SYMPOSIA ON MOLECULAR AND CELLULAR BIOLOGY, APR. 9-15, 1985. J CELL BIOCHEM SUPPL Ø (9 PART C). 1985. 117. CODEN: JCBSD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/85 (Item 1 from file: 399)

116167825 CA: 116(17)167825y PATENT

Methods for in vitro recombination of multigene families for generation of new phenotypes

INVENTOR (AUTHOR): Short, Jay M.; Sorge, Joseph A.

LOCATION: USA

ASSIGNEE: Stratagene

PATENT: PCT International; WO 9116427 A1 DATE: 911031 APPLICATION: WO 91US2910 (910424) *US 513957 (900424)

PAGES: 204 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12N-015/00A; C12P-019/34B; C12P-021/06B; C07H-021/00B DESIGNATED COUNTRIES: AU; CA; FI; JP; KR; NO DESIGNATED REGIONAL: AT; BE; CH; DE; DK; ES; FR; GB; GR; IT; LU; NL; SE

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2/3/86 (Item 2 from file: 399)

106208826 CA: 106(25)208826p JOURNAL

Rapid localization and characterization of random mutations within the 2.mu. circle site-specific recombinase: a general strategy for analysis of protein function

AUTHOR(S): Govind, Nadathur S.; Jayaram, Makkuni LOCATION: Res. Inst. Scripps Clin., La Jolla, CA, 92037, USA JOURNAL: Gene DATE: 1987 VOLUME: 51 NUMBER: 1 PAGES: 31-41 CODEN: GENEDG ISSN: 0378-1119 LANGUAGE: English Copyright 1992 by the American Chemical Society

2/3/87 (Item 3 from file: 399)

104001445 CA: 104(1)1445b JOURNAL

The FLP recombinase of the yeast 2-.mu.m plasmid: characterization of its recombination site

AUTHOR(S): Senecoff, Julie F.; Bruckner, Robert C.; Cox, Michael M. LOCATION: Coll. Agric. Life Sci., Univ. Wisconsin, Madison, WI, 53706, USA

JOURNAL: Proc. Natl. Acad. Sci. U. S. A. DATE: 1985 VOLUME: 62 NUMBER: 21 PAGES: 7270-4 CODEN: PNASA6 ISSN: 0027-8424 LANGUAGE: English

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2/3/88 (Item 4 from file: 399)

102216080 CA: 102(25)216080y JOURNAL

The FLP recombinase of the 2.mu. circle DNA of yeast: interaction with its target sequences

AUTHOR(S): Andrews, Brenda J.; Proteau, Gerald A.; Beatty, Linda G.; Sadowski, Paul D.

LOCATION: Dep. Med. Genet., Univ. Toronto, Toronto, ON, Can., M5S 1A8 JOURNAL: Cell (Cambridge, Mass.) DATE: 1985 VOLUME: 40 NUMBER: 4 PAGES: 795-803 CODEN: CELLB5 ISSN: 0092-8674 LANGUAGE: English

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2/3/89 (Item 1 from file: 434)

11609410 Genuine Article#: HX635 No. References: 12

Title: HALF-SITE STRAND TRANSFER BY STEP-ARREST MUTANTS OF YEAST SITE-SPECIFIC RECOMBINASE FLP

Author(s): SERRE MC: JAYARAM M

Corporate Source: UNIV TEXAS, DEPT MICROBIOL/AUSTIN//TX/78712; UNIV TEXAS, DEPT MICROBIOL/AUSTIN//TX/78712

Journal: JOURNAL OF MOLECULAR BIOLOGY, 1992, V225, N3 (JUN 5), P643-649 Language: ENGLISH Document Type: ARTICLE

2/3/90 (Item 2 from file: 434)

11609409 Genuine Article#: HX635 No. References: 25

Title: HALF-SITE RECOMBINATIONS MEDIATED BY YEAST SITE-SPECIFIC RECOMBINASE-FLP AND RECOMBINASE-R

Author(s): SERRE MC; EVANS BR; ARAKI H; OSHIMA Y; JAYARAM M

Comporate Source: UNIV TEXAS, DEPT MICROBIOL/AUSTIN//TX/78712; UNIV TEXAS, DEPT MICROBIOL/AUSTIN//TX/78712; OSAKA UNIV, FAC ENGN, DEPT FERMENTAT TECHNOL/SUITA/OSAKA 565/JAPAN/

Journal: JOURNAL OF MOLECULAR BIOLOGY, 1992, V225, N3 (JUN 5), P321-642 Language: ENGLISH Document Type: ARTICLE

2/3/91 (Item 3 from file: 434)

11603498 Genuine Article#: HX080 No. References: 40

Title: MUTAGENESIS OF A CONSERVED REGION OF THE GENE ENCODING THE FLP RECOMBINASE OF SACCHAROMYCES-CEREVISIAE - A ROLE FOR ARGININE-191 IN BINDING AND LIGATION

Author(s): FRIESEN H: SADOWSKI PD Corporate Source: UNIV TORONTO, DEPT MOLEC & MED GENET/TORONTO M5S1A8/ONTARIO/CANADA/; UNIV TORONTO.DEPT MOLEC & MED GENET/TORONTO M5S1A8/ONTARIO/CANADA/ Journal: JOURNAL OF MOLECULAR BIOLOGY, 1992, V225, N2 (MAY 20), F313-326 Language: ENGLISH Document Type: ARTICLE 2/3/92 (Item 4 from file: 434) Genuine Article#: HV855 No. References: 41 11588831 Title: SITE-SPECIFIC RECOMBINASE, R, ENCODED BY YEAST PLASMID PSR1 Author(s): ARAKI H; NAKANISHI N; EVANS BR; MATSUZAKI H; JAYARAM M; OSHIMA Y Componate Source: OSAKA UNIV, FAC ENGN, DEPT BIOTECHNOL, 2-1 YAMADAOKA/SUITA/OSAKA 565/JAPAN/; OSAKA UNIV, FAC ENGN, DEPT BIOTECHNOL, 2-1 YAMADAOKA/SUITA/OSAKA 565/JAPAN/; UNIV TEXAS, DEPT MICROBIOL/AUSTIN//TX/78712 Journal: JOURNAL OF MOLECULAR BIOLOGY, 1992, V225, N1 (MAY 5), P25-37 Language: ENGLISH Document Type: ARTICLE 2/3/93 (Item 5 from file: 434) 11506141 Genuine Article#: HN234 No. References: 35 Title: SITE-SPECIFIC RECOMBINATION OF 2-MU-M PLASMID OF YEAST SACCHAROMYCES-CEREVISIAE Author(s): PUSHNOVA EA Corporate Source: ST PETERBURG PEDIAT MED INST/ST PETERBURG//USSR/ Journal: GENETIKA, 1992, V28, N2 (FEB), P25-34 Language: RUSSIAN Document Type: ARTICLE (Abstract Available) 2/3/94 (Item & from file: 434) 11487805 Genuine Article#: HM053 No. References: 33 Title: SITE-SPECIFIC INTEGRATION OF THE HAEMOPHILUS-INFLUENZAE BACTERIOPHAGE HP1 - IDENTIFICATION OF THE POINTS OF RECOMBINATIONAL STRAND EXCHANGE AND THE LIMITS OF THE HOST ATTACHMENT SITE Author(s): HAUSER MA; SCOCCA JJ Corporate Source: JOHNS HOPKINS UNIV, SCH HYG & PUBL HLTH, DEPT BIOCHEM/BALTIMORE//MD/21205; JOHNS HOPKINS UNIV, SCH HYG & PUBL HLTH, DEPT BIOCHEM/BALTIMORE//MD/21205 Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1992, V267, N10 (APR 5), P 6859-6864 Language: ENGLISH Document Type: ARTICLE (Abstract Available) 2/3/95 (Item 7 from file: 434) No. References: 21 11338662 Genuine Article#: HB304 Title: EXCHANGE OF GENE ACTIVITY IN TRANSGENIC PLANTS CATALYZED Y THE CRE-LOX SITE-SPECIFIC RECOMBINATION SYSTEM Author(s): BAYLEY CC; MORGAN M; DALE EC; OW DW Corporate Source: USDA ARS,CTR PLANT GENE EXPRESS,800 BUCHANAN ST/ALBANY//CA/94710; USDA ARS,CTR PLANT GENE EXPRESS,800'BUC: ANAN ST/ALBANY//CA/94710; UNIV CALIF BERKELEY, DEPT PLANT PATHOL/BERKELEY//CA/94720 Journal: PLANT MOLECULAR BIOLOGY, 1992, V18, N2 (JAN), P353-361

2/3/96 (Item 8 from file: 434) 11317754 Genuine Article#: GZ516 No. References: 33

Document Type: ARTICLE (Abstract Available

Language: ENGLISH

Title: A FROG VIRUS-3 GENE CODES FOR A PROTEIN CONTAINING THE MOTIF CHARACTERISTIC OF THE INT FAMILY OF INTEGRASES Author(s): ROHOZINSKI J; GOORHA R Corporate Source: ST JUDE CHILDRENS HOSP, DEFT VIROL & MOLEC BIOL, 332 N LAUDERDALE, FOB 318/MEMPHIS//TN/38101; ST JUDE CHILDRENS HOSP, DEFT VIROL & MOLEC BIOL, 332 N LAUDERDALE, POB 318/MEMPHIS//TN/38101 Journal: VIROLOGY, 1992, V186, N2 (FEB), P693-700 Language: ENGLISH Document Type: ARTICLE 2/3/97 (Item 9 from file: 434) Genuine Article#: EP811 No. References: 61 10583597 Title: A NOVEL RECOMBINATOR IN YEAST BASED ON GENE-II PROTEIN FROM BACTERIOFHAGE-F1 Author(s): STRATHERN JN; WEINSTOCK KG; HIGGINS DR; MCGILL CB Corporate Source: NCI, FREDERICK CANC RES & DEV CTR, BASIC RES PROGRAM/FREDERICK//MD/21701 Journal: GENETICS, 1991, V127, N1, P61-73 Document Type: ARTICLE (Abstract Available) Language: ENGLISH (Item 10 from file: 434) 2/3/98 09323349 Genuine Article#: T4208 No. References: 45 Title: FLP RECOMBINASE OF THE 2-MU-M CIRCLE PLASMID OF SACCHAROMYCES-CEREVISIAE BENDS ITS DNA TARGET - ISOLATION OF FLP MUTANTS DEFECTIVE IN DNA BENDING Author(s): SCHWARTZ CJE; SADOWSKI PD Corporate Source: UNIV TORONTO, DEPT MED GENET/TORONTO M5S 1A8/ONTARIO/CANADA/ Journal: JOURNAL OF MOLECULAR BIOLOGY, 1989, V205, N/, P647-658 Language: ENGLISH Document Type: ARTICLE 2/3/99 (Item 11 from file: 434) 07863892 Genuine Article#: F8861 No. References: 37 Title: ISOLATION OF INTERMEDIATES IN THE BINDING OF THE FLP RECOMBINASE OF THE YEAST PLASMID 2-MIRON CIRCLE TO ITS TARGET SEQUENCE Author(s): ANDREWS BJ; BEATTY LG; SADOWSKI PD Corporate Source: UNIV TORONTO, DEPT MED GENET/TORONTO M5S 1A8/ONTARIO/CANADA/ Journal: JOURNAL OF MOLECULAR BIOLOGY, 1987, V193, N2, P345-358 Language: ENGLISH Document Type: ARTICLE 2/3/100 (Item 12 from file: 434) 07372665 Genuine Article#: C9356 No. References: 23 Title: INTERACTION OF THE FLP RECOMBINASE OF THE SACCHAROMYCES-CEREVISIAE 2-MU-M FLASMID WITH MUTATED TARGET SEQUENCES Author(s): ANDREWS BJ; MCLEOD M; BROACH J; SADOWSKI PD Corporate Source: UNIV TORONTO, DEPT MED GENET/TORONTO M5S 1A8/ONTARIO/CANADA/; COLD SPRING HARBOR LAB/COLD SPRING . HARBOR//NY/11724; PRINCETON UNIV, DEPT MOLEC BIOL/PRINCETON//NJ/08544 Journal: MOLECULAR AND CELLULAR BIOLOGY, 1986, V6, N7, P2482-2489 Language: ENGLISH Document Type: ARTICLE (Item 13 from file: 434) 2/3/101

Genuine Article#: C1205 No. References: 44

Title: FLP SITE-SPECIFIC RECOMBINASE OF YEAST 2-MU-M PLASMID - TOPOLOGICAL

07260459

FEATURES OF THE REACTION

Author(s): BEATTY LG; BABINEAUCLARY D; HOGREFE C; SADOWSKI FD

Corporate Source: UNIV TORONTO, DEPT MED GENET/TORONTO M5S

1A8/ONTARIO/CANADA/

Journal: JOURNAL OF MOLECULAR BIOLOGY, 1986, V188, N4, F529-544

Language: ENGLISH Document Type: ARTICLE

2/3/102 (Item 14 from file: 434)

06806789 Genuine Article#: AUF29 No. References: 22

Title: THE FLP RECOMBINASE OF THE YEAST 2-MU-M PLASMID - CHARACTERIZATION OF ITS RECOMBINATION SITE

Author(s): SENECOFF JF; BRUCKNER RC; COX MM

Corporate Source: UNIV WISCONSIN, COLL AGR & LIFE SCI, DEFT BIOCHEM, 420 HENRY MALL/MADISON//WI/53706

Journal: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, 1985, V82, N21, P7270-7274

Language: ENGLISH Document Type: ARTICLE

2/3/103 (Item 15 from file: 434)

06780315 Genuine Article#: ATE60 No. References: 28

Title: THE FLP RECOMBINASE OF THE SACCHAROMYCES-CEREVISIAE 2-MU-M PLASMID ATTACHES COVALENTLY TO DNA VIA A PHOSPHOTYROSYL LINKAGE

Author(s): GRONOSTAJSKI RM; SADOWSKI PD

Corporate Source: UNIV TORONTO, DEFT MED GENET/TORONTO M5S 1A8/ONTARIO/CANADA/

Journal: MOLECULAR AND CELLULAR BIOLOGY, 1985, V5, N11, P3274-3279

Language: ENGLISH Document Type: ARTICLE

2/3/104 (Item 1 from file: 440)

03761331 Genuine Article#: HZ483 No. References: 12

Title: LIGATION ACTIVITY OF FLP RECOMBINASE - THE STRAND LIGATION ACTIVITY OF A SITE-SPECIFIC RECOMBINASE USING AN ACTIVATED DNA SUBSTRATE

Author(s): PAN GH; SADOWSKI PDV(Reprint)

Corporate Source: UNIV TORONTO, DEPT MOLEC & MED GENET/TORONTO M5S1A8/ONTARIO/CANADA/ (Reprint); UNIV TORONTO, DEPT MOLEC & MED GENET/TORONTO M5S1A8/ONTARIO/CANADA/

Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1992, V267, N18 (JUN 25), P 12397-12399

Language: ENGLISH Document Type: NOTE (Abstract Available)

2/3/105 (Item 1 from file: 76)

1171271 82001618771

Mutations in the 2-.mu.m circle site-specific recombinase that abolish recombination without affecting substrate recognition.

Prasad, P.V.; Young, L.-J.; Jayaram, M.

Dep. Mol. Biol., Res. Inst. Scripps Clin., 10666 N. Torrey Pines Rd., La Jolla, CA 92037, USA

PROC. NATL. ACAD. SCI. USA; 84(8), pp. 2189-2193 1987

Language: English Summary Language: English

2/3/106 (Item 1 from file: 73)

8210454 EMBASE No: 91239554

Erratum: Identification of the active site tyrosine of Flp recombinase. Possible relevance of its location to the mechanism of recombination (Vol.

265 (1990) 18504-18510)

Evans B.R.; Chen J.-W.; Parsons R.L.; Bauer T.K.; Teplow D.B.; Jayaram M. J. BIOL. CHEM. (USA) , 1991, 266/11 (7312) CODEN: JBCHA ISSN: 0021-9258

LANGUAGES: English

2/3/107 (Item 2 from file: 73)

7363228 EMBASE No: 89079376

FLP recombinase of the 2 microm circle plasmid of Saccharomyces cerevisiae bends its DNA target. Isolation of FLP mutants defective in DNA bending

Schwartz C.J.E.; Sadowski P.D.

Department of Medical Genetics, University of Toronto, Toronto, Ont. M5S

J. MOL. BIOL. (United Kingdom) , 1989, 205/4 (647-658) CODEN: JMOBA ISSN: 0022-2836

LANGUAGES: English

2/3/108 (Item 1 from file: 144)

09775158 FASCAL No.: 91-0572331

Domain of a yeast site-specific recombinase (Flp) that recognizes its target site

JING-WEN CHEN; EVANS B R; SANG-HWA YANG; TEPLOW D/ B; JAYARAM M Univ. Texas, dep. microbiology, Austin TX 78712, USA

Journal: Proceedings of the National Academy of Sciences of the United States of America, 1991, 88 (14) 5944-5948

Language: English

2/3/109 (Item 2 from file: 144)

09771721 FASCAL No.: 91-0568894

Protein-based assymmetry and protein-protein interactions in FLP recombinase-mediated site-specific recombination

XIAO-HONG QIAN; INMAN R B; COX M M

Univ. Wisconsin, coll. agricultural life sci., dep. biochemistry, Madison WI 53706, USA

Journal: Journal of biological chemistry (The), 1990, 265 (35) 21779-21788

Language: English

2/3/110 (Item 3 from file: 144)

09730857 FASCAL No.: 91-0527991

Site-specific recombination between homologous chromosomes in Drosophila GOLIC K G

Univ. Chicago, Howard Hughes medical inst., dep; molcular genetics cell biology, Chicago IL 60637, USA

Journal: Science: (Washington, DC), 1991, 252 (5008) 958-961 Language: English

2/3/111 (Item 4 from file: 144) 09563896 PASCAL No.: 91-0354326

Tyr60 variants of Flp recombinase generate conformationally altered protein-DNA complexes : differential activity in full-site and half-site recombinations

JING-WEN CHEN; EVANS B R; LEI ZHENG; JAYARAM M

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Univ. Texas at Austin, dep. microbiology, Austin TX 78712, USA Journal: Journal of molecular biology, 1991, 218 (1) 107-118 Language: English

2/3/112 (Item 5 from file: 144) 07823248 PASCAL No.: 87-0302971

Interaction of the FLF recombinase of the saccharomyces cerevisiae 2 mu m plasmid with mutated target sequences

NDREWS B J; MCLEOD M; BROACH J; SADOWSKI P D

Univ. Toronto, dep. medical genetics, Toronto ON M5S 1A8, Canada Journal: Molecular and cellular biology, 1986, 6 (7) 2482-2489 Language: ENGLISH

2/3/113 (Item 1 from file: 77) 89015048 V17N02

FLP recombinase induction of the breakage-fusion-bridge cycle (BFBC) and gene conversion in Saccharomyces cerevisiae

Rank, G.H.; Xiao, W.; Kolenovsky, A.; Arndt, G.

Univ. Saskatchewan, Saskatoon, Sask., Canada

XVIth International Congress of Genetics 8830579 Toronto (Canada) 20-27 Aug 1988

Genetics Society of Canada; National Research Council Canada; Royal Society of Canada; Biological Council of Canada

The Proceedings of the Congress will be Published in a Special Volume of Journal Genome Poster Paper

2/3/114 (Item 2 from file: 77) 89014585 V17N02

Structure-function relationship of the sequence specific DNA binding function of the FLP recombinase

Amin, A.A.; Sadowski, P.D.

Univ. Toronto, Toronto, Ont., Canada

XVIth International Congress of Genetics 8830579 Toronto (Canada) 20-27 Aug 1988

Genetics Society of Canada; National Research Council Canada; Royal Society of Canada; Biological Council of Canada

The Proceedings of the Congress will be Published in a Special Volume of Journal Genome Poster Paper

2/3/115 (Item 3 from file: 77)

89014584 V17N02

 FLP recombinase of 2 mu circle of S. cerevisiae bends its DNA target: An in vitro analysis

Schwartz, C.J.E.; Sadowski, F.D.

Univ. Toronto, Toronto, Ont., Canada

XVIth International Congress of Genetics 8830579 Toronto (Canada) 20-27 Aug 1988

Genetics Society of Canada; National Research Council Canada; Royal Society of Canada; Biological Council of Canada

The Proceedings of the Congress will be Published in a Special Volume of Journal Genome Poster Paper

2/3/116 (Item 4 from file: 77) 89013277 V17N02 Mutational analysis of the FLP site-specific recombinase of the yeast \mathbf{z}

Sadowski, P.

Univ. Toronto, Toronto, Ont., Canada

XVIth International Congress of Genetics 8830579 Toronto (Canada) 20-27 Aug 1988

Genetics Society of Canada; National Research Council Canada; Royal Society of Canada; Biological Council of Canada

The Proceedings of the Congress will be Published in a Special Volume of Journal Genome

2/3/117 (Item 5 from file: 77)

89012894 V17N02

Step-arrest mutants of FLP recombinase: Implications for the mechanism of recombination

Evans, B.R.; Parsons, R.; Crain, K.; Jayaram, M.

Mol. Biol. Dep., Res. Inst. Scripps Clin. and Res. Found., La Jolla, CA,

14th International Conference on Yeast Genetics and Molecular Biology 8830578 Espoo (Finland) 7-13 Aug 1988

European Association for Cancer Research

Subscription Department C, John Wiley & Sons Inc., 605 Third Avenue, New York, NY 10158 (USA), Abstracts will be Published in Special Issue of Journal 'Yeast' Volume 4. ISSN 0749-503X

2/3/118 (Item 1 from file: 265)

0128688 DIALOG FILE NO. 265/266 FEDERAL RESEARCH IN PROGRESS IDENTIFYING NO.: 5R01GM35654-07 AGENCY CODE: CRISP Site specific recombination in the yeast plasmid 2 micron circle PRINCIPAL INVESTIGATOR: JAYARAM, MAKKUNI ADDRESS: UNIVERSITY OF TEXAS DEPT OF MICROBIOLOGY AUSTIN, TX 78712 PERFORMING ORG.: UNIVERSITY OF TEXAS AUSTIN, AUSTIN, TEXAS SPONSORING ORG.: NATIONAL INSTITUTE OF GENERAL MEDICAL SCIENCES FY: 92 FUNDS: \$265,024

2/3/119 (Item 2 from file: 265)

0092015 DIALOG FILE NO. 265/266 FEDERAL RESEARCH IN PROGRESS
IDENTIFYING NO.: 1R01HD28694-01 AGENCY CODE: CRISP
Site-specific recombination in spermatogenesis (Drosophila)
PRINCIPAL INVESTIGATOR: GOLIC, KENT G
ADDRESS: UNIVERSITY OF UTAH SALT LAKE CITY, UT 84112
PERFORMING ORG.: UNIVERSITY OF UTAH, SALT LAKE CITY, UTAH
SPONSORING ORG.: NATIONAL INSTITUTE OF CHILD HEALTH AND HUMAN DEVELOPMENT
FY: 92 FUNDS: \$152,007

2/3/120 (Item 3 from file: 265)

0019654 DIALOG FILE NO. 265/266 FEDERAL RESEARCH IN PROGRESS
IDENTIFYING NO.: 9105934; 9105934 AGENCY CODE: NSF
Genetic Analysis of Pattern Formation During Drosophila Neurogenesis
PRINCIPAL INVESTIGATOR: Ellis, Hilary M Dr.
PERFORMING ORG.: Emory University, Biology, Atlanta, GA 30322
PROJECT MONITOR: Data is not available
SPONSORING ORG.: National Science Foundation, DIV OF INTEGRATIVE BIOLOGY
& NEUROSCIENC, Washington, D.C., 20550

DATES: 910715 TO 920630 FY: 91 FUNDS: \$69,613 (Item 4 from file: 265) 2/3/121 0019101 DIALOG FILE NO. 265/266 FEDERAL RESEARCH IN PROGRESS IDENTIFYING NO.: 9103946; 9103946 AGENCY CODE: NSF Generation of Mosaicism in Mice by a Site-Specific Recombinase (FLP) PRINCIPAL INVESTIGATOR: O'Gorman, Stephen Dr. PERFORMING ORG.: Salk Institute for Biological Studies, Gene Expression Laboratory, San Diego, CA 92128 PROJECT MONITOR: Thomas E. Brady SPONSORING ORG.: National Science Foundation, DIV OF INTEGRATIVE BIOLOGY & NEUROSCIENC, Washington, D.C., 20550 DATES: 910315 TO 920831 FY: 91 FUNDS: \$49,522 (Item 5 from file: 265) 2/3/122 0016053 DIALOG FILE NO. 265/266 FEDERAL RESEARCH IN PROGRESS IDENTIFYING NO.: 9019220; 9019220 AGENCY CODE: NSF Genetic Analysis in Arabidopsis PRINCIPAL INVESTIGATOR: Signer, Ethan R Dr. PERFORMING Massachusetts Institute of Technology, Biology, ORG.: Cambridge, MA 02139 PROJECT MONITOR: DeLill Nasser SPONSORING ORG.: National Science Foundation, DIV OF MOLECULAR & CELLULAR BIOSCIENCES, Washington, D.C., 20550 DATES: 910201 TO 930731 FY: 91 FUNDS: \$200,000 2/3/123 (Item 1 from file: 35) 01212062 ORDER NO: AADNN-59965 THE ROLE OF DNA BENDING IN FLP-MEDIATED SITE-SPECIFIC RECOMBINATION Author: SCHWARTZ, CAROL JUDITH ELAINE Degree: PH.D. Year: 1990 Corporate Source/Institution: UNIVERSITY OF TORONTO (CANADA) (0779) Source: VOLUME 52/11-B OF DISSERTATION ABSTRACTS INTERNATIONAL. PAGE 5647. 209 PAGES ISBN: 0-315-59965-0 2/3/124 (Item 2 from file: 35) 01142876 ORDER NO: AAD90-30816 UNUSUAL DNA STRUCTURE IN SITE-SPECIFIC AND HOMOLOGOUS RECOMBINATION (RECOMBINATION) Author: UMLAUF, SCOTT W. Degree: PH.D. Year: 1990 Corporate Source/Institution: THE UNIVERSITY OF WISCONSIN - MADISON (Source: VOLUME 51/09-B OF DISSERTATION ABSTRACTS INTERNATIONAL. PAGE 4199. 219 PAGES (Item 3 from file: 35) 2/3/125

ANALYSIS OF THE MAJOR DNASE I HYPERSENSITIVE SITE ON THE YEAST TWO-MICRON

1061565 ORDER NO: AAD89-12817

Author: STRAND, ANDREW DAVID

DNA PLASMID

Degree: PH.D. Year: 1989

Corporate Bource/Institution: UNIVERBITY OF MINHEBOTA (0130) Source: VOLUME 50/02-B OF DISSERTATION ABSTRACTS INTERNATIONAL.

PAGE 446. 111 PAGES

2/3/126 (Item 4 from file: 35)

949308 ORDER NO: AAD87-06690

A GENETIC ANALYSIS OF FACTORS INVOLVED IN THE MAINTENANCE OF THE 2 MICRON PLASMID OF SACCHAROMYCES CEREVISIAE (CHROMATIN)

Author: VEIT, BRUCE EDWARD

Degree: PH.D. Year: 1986

Corporate Source/Institution: UNIVERSITY OF WASHINGTON (0250)
Source: VOLUME 47/12-B OF DISSERTATION ABSTRACTS INTERNATIONAL.
PAGE 4763. 97 PAGES

2/3/127 (Item 1 from file: 51) 00405585 91-03-b0028 SUBFILE: FSTA

Yeast 2 MUm vectors replicate and undergo recombination in Torulaspora delbrueckii.

Compagno, C.; Ranzi, B. M.; Martegani, E.

Correspondence (Reprint) address, B. M. Ranzi, Dipartimento di Fisiologia e Biochimica Generali, Sezione di Biochimica Comparata, Univ. di Milano, Milan, Italy

Molecular Microbiology 1989 , 3 (8) 1003-1010 LANGUAGE: English

2/3/128 (Item 1 from file: 60)

09154644

PROJ NO: NYC-186301 AGENCY : SAES NY.C

PROJ TYPE: STATE

START: 01 JUL 91 TERM: 30 JUN 92

INVEST: MACINTYRE R J

ENTOMOLOGY

CORNELL UNIVERSITY ITHACA NEW YORK 14853

DEVELOPMENT OF A MORE EFFICIENT INSECT TRANSFORMATION SYSTEM

OBJECTIVES: The goal of the research described below is to develop a system in which DNA canbe both easily and effectively delivered to insect embryos and, using the yeast "flip recombinase" system, insure the recovery of transgenic animals at high frequencies.

PRIMARY HEADINGS: R207 Insect Control-Field Crops; A4500 Protection Against Insects; C6500 Invertebrates; F1313 Physiology-Other

2/3/129 (Item 2 from file: 60)

09091400

PROJ NO: WISØ2827 AGENCY : SAES WIS

PROJ TYPE: STATE

START: 01 JUL 86 TERM: 30 NOV 96 FY: 1989

INVEST: COX M M

BIOCHEMISTRY UNIV OF WISCONSIN MADISON WISCONSIN 53706

?t3/3/1-3

THE BIOCHEMISTRY OF GENETIC RECOMBINATION

OBJECTIVES: The FLP recombinase (derived from yeast) has been purified extensively. The properties of this protein and the recombination event it catalyzes are being studied in vitro. The recombination site utilized by this protein has been defined in detail. Studies on the mechanism of action of this recombination system are now getting underway.

PRIMARY HEADINGS: R318 Noncommodity Biotechnology, Biometry; A7000 Experimental Design, Statistical Methods; C6300 Biological Cell Systems; F0114 Biochemistry and Biophysics-Other

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2/3/130
             (Item 1 from file: 286)
0050984
          Journal Announcement: 08APR91
                                          Doc Type: 2
  Nature, 15 MAR 1991, Vol(No) 251(4999), Page(s) 1351-1355
1ST COMPANY/ORGANIZATION NAME:
  Salk Institute for Biological Studies, The, USA (1921)
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        Items
                Description
S1
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S2
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               3 S2 AND MAMMAL?
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3/3/1 (Item 1 from file: 155)

07645850 91164850

Recombinase-mediated gene activation and site-specific integration in mammalian cells.

O'Gorman S; Fox DT; Wahl GM

Gene Expression Laboratory, Salk Institute for Biological Studies, La Jolla, CA 92037.

Science Mar 15 1991, 251 (4999) p1351-5, ISSN 0036-8075

Journal Code: UJ7 Languages: ENGLISH

Document type: JOURNAL ARTICLE

3/3/2 (Item 1 from file: 434)

11338662 Genuine Article#: HB304 No. References: 21

Title: EXCHANGE OF GENE ACTIVITY IN TRANSGENIC PLANTS CATALYZED BY THE CRE-LOX SITE-SPECIFIC RECOMBINATION SYSTEM

Author(s): BAYLEY CC; MORGAN M; DALE EC; OW DW

Corporate Source: USDA ARS,CTR PLANT GENE EXPRESS,800 BUCHANAN ST/ALBANY//CA/94710; USDA ARS,CTR PLANT GENE EXPRESS,800 BUCHANAN ST/ALBANY//CA/94710; UNIV CALIF BERKELEY,DEPT PLANT PATHOL/BERKELEY//CA/94720

Journal: PLANT MOLECULAR BIOLOGY, 1992, V18, N2 (JAN), P353-361 Language: ENGLISH Document Type: ARTICLE (Abstract Available)

3/3/3 (Item 1 from file: 286)
0050984 Journal Announcement: 08APR91 Doc Type: 2
Nature, 15 MAR 1991, Vol(No) 251(4999), Page(s) 1351-1355

1ST COMPANY/ORGANIZATION NAME:

Salk Institute for Biological Studies, Th., USA (1921) ?t3/4/1-3

3/4/1 (Item 1 from file: 155)

FN- DIALOG MEDLINE file 155

AN- 076458501

AN- (NLM) 911648501

TI- Recombinase-mediated gene activation and site-specific integration in mammalian cells.

AU- O'Gorman S; Fox DT; Wahl GMI

CS- Gene Expression Laboratory, Salk Institute for Biological Studies, La Jolla, CA 92037.1

JN- Science; 251 (4999) p1351-51

PY- Mar 15 19911

SN- 0036-80751

JC- UJ71

LA- ENGLISHI

DT- JOURNAL ARTICLE!

JA- 91061

SF- INDEX MEDICUS!

AB- A binary system for gene activation and site-specific integration, based on the conditional recombination of transfected sequences mediated by the FLP recombinase from yeast, was implemented in mammalian cells. In several cell lines, FLP rapidly and precisely

recombined copies of its specific target sequence to activate an otherwise silent beta-galactosidase reporter gene. Clones of marked cells were generated by excisional recombination within a chromosomally integrated copy of the silent reporter. By the reverse reaction, integration of transfected DNA was targeted to a specific chromosomal site. The results suggest that FLP could be used to mosaically activate or inactivate transgenes for analysis of vertebrate development, and to efficiently integrate transfected DNA at predetermined chromosomal locations.!

GS- Animal; In Vitro; Support, Non-U.S. Gov'tl

DE- *DNA Nucleotidyltransferases -- Metabolism -- ME;

**Mammals -- Genetics -- GE; **Recombination, Genetic; **Transfection;

beta-Galactosidase -- Genetics -- GE; *Animals, Transgenic; *Cell Line;

**DNA Nucleotidyltransferases -- Genetics -- GE; *Restriction Mapping!

ID- EC 2.7.7.- (DNA Nucleotidyltransferases); EC 2.7.7.- (FLP recombinase); EC 3.2.1.23 (beta-Galactosidase);

ID- FLPI

3/4/2 (Item 1 from file: 434)

FN- SCISEARCH_1974 - 9206W3

AN- 113386621

GA- HB3041

TI- EXCHANGE OF GENE ACTIVITY IN TRANSGENIC PLANTS CATALYZED BY THE CRE-LOX SITE-SPECIFIC RECOMBINATION SYSTEM!

LA- ENGLISHI

AU- BAYLEY CC; MORGAN M; DALE EC; OW DWI

CS- USDA ARS,CTR PLANT GENE EXPRESS,800 BUCHANAN ST/ALBANY//CA/94710; USDA ARS,CTR PLANT GENE EXPRESS,800 BUCHANAN ST/ALBANY//CA/94710; UNIV CALIF BERKELEY,DEPT PLANT PATHOL/BERKELEY//CA/94720|

GI - USAT

JN- PLANT MOLECULAR BIOLOGY, 1992, V18, N2, P353-3611

PY- 19921

DT- ARTICLE!

NR- 211

SF- SciSearch; CC LIFE--Current Contents, Life Sciences; CC AGRI--Current Contents, Agriculture, Biology & Environmental Sciences!

SC- BOTANY; BIOCHEMISTRY & MOLECULAR BIOLOGY!

AB- The Cre-lox site-specific recombination system of bacteriophage P1 was used to excise a firefly luciferase (luc) gene which had previously been incorporated into the tobacco genome. The excision event was due to site-specific DNA recombination between two lox sequences flanking the luc gene and was catalyzed by the Cre recombinase introduced by cross-fertilization. Recombination resulted in the fusion of a promoter with a distally located hygromycin phosphotransferase (hpt) coding sequence and the excision event was monitored as a phenotypic change from expression of luc to expression of hpt. The efficiency of recombination was estimated from the exchange of gene activity and confirmed by molecular analysis. The relevance to potential applications of site-specific deletion-fusion events for chromosome engineering are discussed.

DE- Author Keywords: GENETIC ENGINEERING; PHAGE P1; RECOMBINASE; LUCIFERASE; SELECTABLE MARKERS!

ID- KeyWords Plus: FIREFLY LUCIFERASE GENE; FLP RECOMBINASE;
MAMMALIAN-CELLS; 2-MU CIRCLE; DNA; YEAST; BACTERIOPHAGE-P1;

GENOME: EXPRESSION: SEQUENCES! (TRANSGENIC PLANTS; TRANSIENT EXPRESSION OF THE GUS GENE; RF- 90-0047 002 INDICA RICE PROTOPLASTS; MICROPROJECTILE BOMBARDMENT; AGROBACTERIUM MEDIATED TRANSFORMATION) 90-1257 001 (BACILLUS-THURINGIENSIS STRAINS; TRANSGENIC TOBACCO PLANTS; DRY BEANS (PHASEOLUS-VULGARIS L); EXPRESSION OF INSECTICIDAL ACTIVITY: INSECT MIDGUT) 90-2362 001 (STA58 MAJOR ANTIGEN GENE; RHODOCOCCUS-FASCIANS CLONING VECTORS; ESCHERICHIA-COLI CHROMOCOME; PRECISE IDENTIFICATION) 90-4791 001 (FIREFLY LUCIFERASE EXPRESSION IN TRANSGENIC PLANTS; PROTEIN OF MAIZE TRANSPOSABLE ELEMENT AC: CAULIFLOWER MOSAIC-VIRUS; REPORTER GENES) 90-7783 001 (POLYMERASE CHAIN-REACTION; DNA AMPLIFICATION; POLYMORPHIC NUCLEOTIDE SUBSTITUTIONS IN TETA-GLOBIN GENES) CR - ANDREWS BJ, 1985, V40, P795, CELL BEVAN M, 1984, V12, P8711, NUCLEIC ACIDS RES BROACH JR, 1980, V21, P501, CELL CRAIG NL, 1988, V22, P77, ANNU REV GENET DALE EC, 1990, V91, P79, GENE DEWET JR, 1987, V7, P725, MOL CELL BIOL GOLIC KG, 1989, V59, P499, CELL HOESS RH, 1985, V181, P351, J MOL BIOL HORSCH RB, 1985, V227, P1229, SCIENCE KASTER KR, 1983, V11, P6895, NUCLEIC ACIDS RES MANIATIS T, 1982, MOL CLONING ODELL J, 1990, V223, P369, MOL GEN GENET OGORMAN S, 1991, V251, P1351, SCIENCE

SENECOFF JF, 1985, V82, P7270, P NATL ACCD SCI USA STERNBERG N, 1981, V150, P467, J MOL BIO! VAECK M, 1987, V328, P33, NATURE VERWOERD TC, 1989, V17, P2362, NUCLEIC ACIDS RESIL

SAUER B, 1989, V17, P147, NUCLEIC ACIDS LES SAUER B, 1988, V85, P5166, P NATL ACAD SCI USA

OW DW, 1986, V234, P856, SCIENCE SAIKI RK, 1988, V239, P487, SCIENCE

mosaically

3/4/3 (Item 1 from file: 286)

FM- DIALOG File 286: 286

AM- 00509841

JA- 08APR911

DT- 21

JM- Nature, 15 MAR 1991, Vol(No) 251(4999), Page(s) 1351-13551

AM- Salk Institute scientists have shown that the site specific recombinase enzyme, FLP, from Saccharomyces cere isiae can be used for gene activation in mammalian cells and have suggested it may be useful to

integrate transfected DNA at predetermined chromosomal locations.! Cm- Salk Institute for Biological Studies, The, USA (1921)! ?logoff

inactivate

or activate ransgenes or to efficiently

=> d his

(FILE 'USPAT' ENTERED AT 09:57:49 ON 12 JUL 94) SET PAGELENGTH SCROLL

L1 5 S (YEAST? OR CEREVISIAE?)(30A)(FRT OR FLP OR RECOMBINASE?)

=> d 1-5

- 1. 5,268,296, Dec. 7, 1993, DNA vector and recombinant host cell for production of hirullin P6 and P18; Reinhard Maschler, et al., 435/252.3, 69.1, 172.3, 320.1, 942; 536/23.5 [IMAGE AVAILABLE]
- 2. 5,268,285, Dec. 7, 1993, Strains of yeast with increased rates of glycolysis; David T. Rogers, et al., 435/172.3, 161, 194, 254.21, 320.1 [IMAGE AVAILABLE]
- 3. 5,227,288, Jul. 13, 1993, DNA sequencing vector with reversible insert; Frederick R. Blattner, 435/6, 252.3, 252.33, 320.1; 935/29, 72, 73 [IMAGE AVAILABLE]
- 4. 5,114,922, May 19, 1992, Polypeptides with an anticoagulant activity; Reinhard Maschler, et al., 514/12; 530/324 [IMAGE AVAILABLE]
- 5. 4,997,757, Mar. 5, 1991, Process for detecting potential carcinogens; Robert H. Schiestl, 435/172.1, 6, 29, 172.3; 935/76, 78, 79, 84 [IMAGE AVAILABLE]

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=> d his 12

(FILE 'USPAT' ENTERED AT 09:57:49 ON 12 JUL 94) L2 LS MAMMAL?(100A)(FRT OR FLP OR RECOMBINASE?)

⇔ d kwie

US PAT NO: 5,159,066 [IMAGE AVAILABLE]

L2: 1 of 1

ABSTRACT:

Recombination activating gene of mammalian origin (RAG-1), cDNA of RAG-1 of mammalian origin, mRNA expressed by RAG-1, the encoded recombinase and antibodies specific for the recombinase, as well as the use of the same for a diagnostic or therapeutic purpose.

DETDESC:

DETD(2)

The present invention relates to a gene of mammalian origin, referred to as recombination activating gene or RAG-1, which confers the ability to carry out V(D)J recombination on cells in which it is expressed. The RAG-1 gene product is thus a direct or indirect activator of V(D)J recombinase activity. The invention also refers to RAG-1 mRNA and to the RAG-1 encoded product. RAG-1 has been shown in pre-B. . . as in all transfectants into which it has been introduced. This pattern of expression is that expected for the V(D)J recombinase and, therefore, RAG-1 appears to be a master controller of the development of the effector cells of the immune system. .

CLAIMS:

CLMS(3)

3. Isolated DNA of mammalian origin encoding recombinase.

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  (FILE 'USPAT' ENTERED AT 14:51:48 ON 03 FEB 94)
       SET PAGELENGTH SCROLL
       0 S MAMMAL?(20A)(FLP OR FRT)(20A)(TRANSFECT? OR TRANSFORM? OR R
L1
       5 S YEAST(20A)(FRT OR FLP)
L2
L3
       0 S MAMMAL?(50A)(FLP OR FRT)
       0 S MAMMAL?(100A)(FRT OR FLP)
L4
L5
       0 S MAMMAL(50A)(YEAST OR CEREVISIAE)(50A)RECOMBINASE?
L6
       0 S MAMMAL?(200A)(YEAST? OR FUNG? OR CEREVISIAE)(200A)RECOMBINA
=> file jpoabs
FILE 'JPOABS' ENTERED AT 14:58:17 ON 03 FEB 94
    JAPANESE PATENT ABSTRACTS
 * CURRENTLY, DATA IS LOADED THROUGH THE ABSTRACT PUBLICATION *
 * DATE OF JULY 5, 1993
 * THE LATEST GROUPS RECEIVED ARE: C1078 E1392, M1438 & P1567. *
=> s l1
     769 MAMMAL?
     21 FLP
     12 FRT
     32 TRANSFECT?
    39194 TRANSFORM?
    2791 RECOMB?
       0 MAMMAL?(20A)(FLP OR FRT)(20A)(TRANSFECT? OR TRANSFORM? OR RECO
L7
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    2510 YEAST
     12 FRT
     21 FLP
L8
       0 YEAST(20A)(FRT OR FLP)
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     769 MAMMAL?
     21 FLP
      12 FRT
L9
       0 MAMMAL?(50A)(FLP OR FRT)
=> s |4
     769 MAMMAL?
     12 FRT
     21 FLP
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L10

0 MAMMAL?(100A)(FRT OR FLP)

=> s I5
355 MAMMAL
2510 YEAST
278 CEREVISIAE
0 RECOMBINASE?
L11 0 MAMMAL(50A)(YEAST OR CEREVISIAE)(50A)RECOMBINASE?

=> log y U.S. Patent & Trademark Office LOGOFF AT 14:58:54 ON 03 FEB 94 mammal? (100 N)(FLP or FRT)

DIAL OBJECT OF OPPORT

? t2/7/1-16

2/7/1 (Item 1 from file: 434)

12729441 Genuine Article#: MK280 Number of References: 51

Title: SITE-SPECIFIC RECOMBINASES - TOOLS FOR GENOME ENGINEERING

Author(s): KILBY NJ; SNAITH MR; MURRAY JAH

Corporate Source: UNIV CAMBRIDGE, INST BIOTECHNOL, TENNIS COURT

RD/CAMBRIDGE

CB2 1QT//ENGLAND/

Journal: TRENDS IN GENETICS, 1993, V9, N12 (DEC), P413-421

ISSN: 0168-9525

Language: ENGLISH Document Type: REVIEW

Abstract: Site-specific recombinases, from bacteriophage and yeasts have been developed as novel tools for manipulating DNA both in the test-tube and in living organisms. We discuss the characteristics of these enzyme systems, review their application in genetic and developmental studies and speculate on their future potential for large-scale directed modifications of eukaryotic genomes.

2/7/2 (Item 2 from file: 434)

12101712 Genuine Article#: KM161 Number of References: 24

Title: LIGATION OF SYNTHETIC ACTIVATED DNA SUBSTRATES BY SITE-SPECIFIC RECOMBINASES AND TOPOISOMERASE-I

Author(s): PAN GH; LUETKE K; JUBY CD; BROUSSEAU R; SADOWSKI P Corporate Source: UNIV TORONTO, DEPT MOLEC & MED GENET/TORONTO M5S1A8/ONTARIO/CANADA/; UNIV TORONTO, DEPT MOLEC & MED GENET/TORONTO

M5S1A8/ONTARIO/CANADA/; NATL RES COUNCIL CANADA, BIOTECHNOL RES INST, GENET ENGN SECT/MONTREAL H4P 2R2/QUEBEC/CANADA/

Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1993, V268, N5 (FEB 15), P 3683-3689

ISSN: 0021-9258

Language: ENGLISH Document Type: ARTICLE

Abstract: The FLP protein of the 2-mum plasmid of Saccharomyces cerevisiae is a conservative site-specific recombinase that is involved in the amplification of the plasmid. This recombination reaction proceeds via the covalent attachment of the protein to the 3'-phosphoryl group at the site of the breaks through a phosphotyrosine linkage. We have recently developed an assay that measures FLP-mediated strand ligation independent of FLP-mediated cleavage and covalent attachment to the DNA. The substrate for ligation was produced by FLP-induced cleavage of the FLP recognition site followed by digestion with Pronase and was shown to contain (at least) a tyrosine residue at the 3'-PO4 terminus adjacent to the FLP cleavage sites.

We have now synthesized artificial substrates that bear a tyrosine residue on the 3'-PO4 of an appropriate oligonucleotide and find that this substrate is ligated as efficiently as the previous ligation substrates that were isolated after FLP cleavage of the substrate. Analogous substrates for other members of the integrase family of recombinases (lambda integrase protein, P1-Cre protein) as well as for mammalian topoisomerase I are also active as ligation substrates with their cognate protein. This class of activated substrates should be

2/7/3 (Item 3 from file: 434)

11338662 Genuine Article#: HB304 Number of References: 21

Title: EXCHANGE OF GENE ACTIVITY IN TRANSGENIC PLANTS CATALYZED BY THE

CRE-LOX SITE-SPECIFIC RECOMBINATION SYSTEM

Author(s): BAYLEY CC; MORGAN M; DALE EC; OW DW

Corporate Source: USDA ARS,CTR PLANT GENE EXPRESS,800 BUCHANAN ST/ALBANY//CA/94710; USDA ARS,CTR PLANT GENE EXPRESS,800 BUCHANAN ST/ALBANY//CA/94710; UNIV CALIF BERKELEY,DEPT PLANT PATHOL/BERKELEY//CA/94720

Journal: PLANT MOLECULAR BIOLOGY, 1992, V18, N2 (JAN), P353-361

Language: ENGLISH Document Type: ARTICLE

Abstract: The Cre-lox site-specific recombination system of bacteriophage P1 was used to excise a firefly luciferase (luc) gene which had previously been incorporated into the tobacco genome. The excision event was due to site-specific DNA recombination between two lox sequences flanking the luc gene and was catalyzed by the Cre recombinase introduced by cross-fertilization. Recombination resulted in the fusion of a promoter with a distally located hygromycin phosphotransferase (hpt) coding sequence and the excision event was monitored as a phenotypic change from expression of luc to expression of hpt. The efficiency of recombination was estimated from the exchange of gene activity and confirmed by molecular analysis. The relevance to potential applications of site-specific deletion-fusion events for chromosome engineering are discussed.

2/7/4 (Item 4 from file: 434)

10707719 Genuine Article#: FB733 Number of References: 25

Title: RECOMBINASE-MEDIATED GENE ACTIVATION AND SITE-SPECIFIC INTEGRATION

TEORATION CELL

IN MAMMALIAN-CELLS

Author(s): OGORMAN S; FOX DT; WAHL GM

Corporate Source: SALK INST BIOL STUDIES, GENE EXPRESS LAB/LA

JOLLA//CA/92037

Journal: SCIENCE, 1991, V251, N4999, P1351-1355

Language: ENGLISH Document Type: ARTICLE

Abstract: A binary system for gene activation and site-specific integration, based on the conditional recombination of transfected sequences mediated by the FLP recombinase from yeast, was implemented in mammalian cells. In several cell lines, FLP rapidly and precisely recombined copies of its specific target sequence to activate an otherwise silent beta-galactosidase reporter gene. Clones of marked cells were generated by excisional recombination within a chromosomally integrated copy of the silent reporter. By the reverse reaction, integration of transfected DNA was targeted to a specific chromosomal site. The results suggest that FLP could be used to mosaically activate or inactivate transgenes for analysis of vertebrate development, and to efficiently integrate transfected DNA at predetermined chromosomal locations.

2/7/5 (Item 5 from file: 434)

10161463 Genuine Article#: DE904 Number of References: 75

Title: A SITE-SPECIFIC SELF-CLEAVAGE REACTION PERFORMED BY A NOVEL RNA IN

NEUROSPORA MITOCHONDRIA Author(s): SAVILLE BJ; COLLINS RA

Corporate Source: UNIV TORONTO, DEPT BOT/TORONTO M5S

3B2/ONTARIO/CANADA/;

UNIV TORONTO, CTR PLANT BIOTECHNOL/TORONTO M5S

3B2/ONTARIO/CANADA/

Journal: CELL, 1990, V61, N4, P685-696

Language: ENGLISH Document Type: ARTICLE

2/7/6 (Item 1 from file: 357)

142790 DBA Accession No.: 93-00842

Gene transfer - gene transmission by retro virus vector, yeast artificial chromosome, mouse zygote homologous recombination, Cre-recombinase method and Flp system (conference abstract)

AUTHOR: Wagner E F

CORPORATE SOURCE: Research Institute of Molecular Pathology (IMP), Dr Bohr-Gasse 7, A-1030, Vienna, Austria.

JOURNAL: Science (258, Suppl., 31-32) 1992 CODEN: SCIEAS

LANGUAGE: English

ABSTRACT: Applications and limitations of gene transfer techniques were discussed. The high efficiency of retro virus infection allows the introduction of genes into cells, e.g. hematopoietic cells. These viral systems provide a method for the generation of animal models for human blood diseases and for possible gene therapy applications. However, the use of yeast artificial chromosomes introduced into cells via DNA-lipid micelles, or the generation of large transgenes through homologous recombination in mouse zygotes, provide a much superior gene transfer system to viral vector systems. Gene transfer techniques are also being used to inactivate a given gene locus by gene targeting. Two new loss-of-function approaches have recently been developed: (1) using the Cre- recombinase; and (2) using the Flp system. These 2 new methods may allow tissue-specific and developmentally regulated gene inactivation in transgenic mice as a function of the site-specific recombinase action. (7 ref)

2/7/7 (Item 2 from file: 357)

141482 DBA Accession No.: 92-13974 PATENT

FLP-mediated gene modification in mammalian cell - vector with FLP-recombinase gene and recombination site for e.g. gene targeting, gene therapy or transgenic animal development research

PATENT ASSIGNEE: Salk-Inst.Biol.Stud. 1992

PATENT NUMBER: WO 9215694 PATENT DATE: 920917 WPI ACCESSION NO.: 92-331739 (9240)

PRIORITY APPLIC. NO.: US 666252 APPLIC. DATE: 910308 NATIONAL APPLIC. NO.: WO 92US1899 APPLIC. DATE: 920306

LANGUAGE: English

ABSTRACT: A new mammalian recombination system comprises Saccharomyces cerevisiae FLP-recombinase (or a gene encoding it) and DNA containing at least 1 FLP recombination target site. The following are also new:

DNA containing at least 1 FLP recombination site, at least 1 restriction site, at least 1 selectable marker, a bacterial (and optionally a mammal or virus) replication origin; the new DNA inserted

into the FLP recombination target site, and with a 2nd FLP target site in tandem with the 1st; methods for assembly of functional genes for activation of expression in mammal cells, disrupting gene expression in a mammal cells, recovery of transfected DNA from the genome of a transfected organism, and precisely targeted integration of DNA into the genome of a host, all using FLP-recombinase; a transgenic non-human mammal containing at least 1 FLP recombination site in its genome; a method for analysis of mammal development, using the above transgenic mammal and a vector encoding FLP under the control of a conditional promoter, and a reporter gene. The system may also be useful in gene therapy. (49pp)

2/7/8 (Item 3 from file: 357)

089171 DBA Accession No.: 89-07162

Production and isolation of large quantities of monoclonal antibody using serum-free medium and fast protein liquid chromatography - hybridoma cell culture

AUTHOR: Stocks S J; +Brooks D E

CORPORATE SOURCE: Department of Pathology, 2211 Wesbrook Mall, Vancouver, V6T 1W5, Canada.

JOURNAL: Hybridoma (8, 2, 241-47) 1989 CODEN: HYBRDY

LANGUAGE: English

ABSTRACT: A method for the production and purification of monoclonal antibody (MAb) on a large scale is described. 2 Hybridoma lines were used to generate monoclonal antibodies in serum-free medium; a rat-rat hybridoma specific for a surface antigen of a hybrid mouse cell line, and a mouse-mouse hybridoma line specific for rat IgG2a. The serum free medium (RPM1-1640) was supplemented with 5 ug/ml cattle insulin, and incubation was at 37 deg. Both hybridoma lines became confluent within 10 days at maximum cell density. Large-quantities of MAbs were produced in the medium, and purification was easily accomplished within a working day at 4 deg to retain high MAb activity. Ammonium sulfate precipitation, which can cause activity loss, was avoided. The serum free medium was purified by ultrafiltration through an Amicon XM100A filter and fast protein liquid chromatography on a mono Q column with an ionic strength and pH elution gradient. Yields obtained were between 10-30 mg pure MAb/l. (13 ref)

2/7/9 (Item 1 from file: 149)

10844741 Dialog File 149: Health Periodicals Database

Use Format 9 for FULL TEXT

TITLE: Site-specific recombination between homologous chromosomes in Drosophila.

AUTHOR: Golic, Kent G.

JOURNAL: Science VOL.: v252 ISSUE: n5008 PAGINATION: p958(4)

PUBLICATION DATE: May 17, 1991

AVAILABILITY: FULL TEXT Online LINE COUNT: 00224

SOURCE FILE: MI File 47

2/7/10 (Item 1 from file: 399)

118074746 CA: 118(9)74746z PATENT

Site-specific integration and excision of transforming DNA in animal cells using the Flp recombinase of yeast

INVENTOR(AUTHOR): Wahl, Geoffrey M.; O'Gorman, Stephen V.

LOCATION: USA ASSIGNEE: Salk Institute for Biological Studies PATENT: PCT International; WO 9215694 A1 DATE: 920917 APPLICATION: WO 92US1899 (920306) *US 666252 (910308) PAGES: 54 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12N-015/85A; C12N-005/16B; C07H-015/12B DESIGNATED COUNTRIES: CA; JP DESIGNATED REGIONAL: AT; BE; CH; DE; DK; ES; FR; GB; GR; IT; LU; MC; NL; SE SECTION: CA203001 Biochemical Genetics IDENTIFIERS: recombination transforming DNA flp recombinase **DESCRIPTORS:** Development, mammalian... anal. of, developmental regulation of reporter genes in, recombination of transforming DNA using flp recombinase in relation to Genetic element, promoter... developmentally regulated, expression of reporter genes from, recombination of transforming DNA using flp recombinase in relation to Animal cell line, CV-1... Animal cell line, F9... Animal cell line, 293... expression in, of gene for flp recombinase, site-specific recombination of transforming DNA in relation to Enzymes, DNA-recombining... flp, gene for, expression in animal cells of, for site-specific integration or excision of transforming DNA Saccharomyces cerevisiae... Saccharomyces... flp recombinase of, gene for, expression in animal cells of, for site-specific integration or excision of transforming DNA Gene.microbial... for flp recombinase, expression in animal cell culture of, for site-specific integration or excision of transforming DNA Genetic element... frt (flp recombinase target site), site-specific recombination of transforming DNA in animal cells via, expression of flp recombinase

gene in relation to

Animal cell...

mammalian, site-specific recombination of transforming DNA in, flp recombinase and frt sites in

Deoxyribonucleic acid sequences...

of flp recombinase gene of Saccharomyces cerevisiae Protein sequences...

of flp recombinase of Saccharomyces cerevisiae

Recombination, genetic, site-specific... Recombination, genetic, site-specific excisive...

of transforming DNA in animal cell culture, flp recombinase and frt sites in

Mammal...

transgenic, site-specific recombination of transforming DNA in, flp recombinase and frt sites in

CAS REGISTRY NUMBERS:

145752-47-2 amino acid sequence of, complete, and expression in animal cell culture of gene for

145752-45-0 nucleotide sequence of

145752-46-1 nucleotide sequence of, complete, and expression in animal cell culture of

145752-44-9 nucleotide sequence of, in transforming DNA for site-specific recombination of transforming DNA

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2/7/11 (Item 1 from file: 265)
0103231 DIALOG FILE NO. 265/266 FEDERAL RESEARCH IN PROGRESS
IDENTIFYING NO.: 1R01HD30255-01 AGENCY CODE: CRISP
FATE MAPS OF EMBRYONIC GENE EXPRESSION IN MICE
PRINCIPAL INVESTIGATOR: O'GORMAN, STEPHEN V
ADDRESS: SALK INSTITUTE PO BOX 85800 SAN DIEGO, CA 92186-5800
PERFORMING ORG.: SALK INSTITUTE FOR BIOLOGICAL STUDIES, SAN

CALIFÓRNIA

DIEGO.

SPONSORING ORG.: NATIONAL INSTITUTE OF CHILD HEALTH AND HUMAN DEVELOPMENT

FY: 93 FUNDS: \$260,269 TYPE OF AWARD: New Award (Type 1) SUMMARY: The long term objective of the research initiated by this proposal is to investigate the genetic regulation of mammalian development. The principal experimental objective is to compile fate maps of the mature fates of cells that descend from progenitors that transiently express specific candidate mammalian developmental control genes during embryonic and fetal stages in transgenic mice. This will be done both in normal mice, and in mice that fail to express the normal products of genes of interest. A novel molecular paradigm for fate mapping will be employed that is based on the precise recombination of transgenes by the yeast recombinase FLP. By this means, the transient activity of a gene can be used to indelibly mark not only the cells in which the gene is expressed, but all of its descendants, even if the latter do not express the gene.

The specific aims of this proposal are to define the descendant domains (lineages) established by progenitors that transiently express Hox 2.9. Krox 20, or Hox 2.6 in the hindbrain and adjacent branchial arch tissues in both normal animals and in, animals that fail to express the normal products of these genes. Both the descendant expression domains and the descendant functional domains of these genes will be mapped and distinguished from one another. The first product of the research program will be a fate map of the mouse that correlates early patterns of gene expression with the organization of cells and tissues in the mature, normal animal. The second product will be a knowledge of whether, and if so how, these fates are altered when the gene of interest is not expressed. They will additionally address the question of compartmentation in the mammalian hindbrain and branchial arches. The maps of normal and mutant cell fates will enormously increase our understanding of the roles played by individual genes in the intricate genetic program that regulates mammalian development, and additionally provide a wealth of new information about cell proliferation, cell mixing, and cell migration in the mammalian embryo. In this manner, the research program will contribute to an improved understanding of normal mammalian development and to the kinds of developmental deficits that arise from alterations in specific gene products.

2/7/12 (Item 1 from file: 286) 0050984 Journal Announcement: 08APR91 Doc Type: 2 Nature, 15 MAR 1991, Vol(No) 251(4999), Page(s) 1351-1355

PRIORITY DATE (DEMAND FOR INTERNATIONAL APPL. FILED PRIOR TO EXPIRATION OF 19TH MONTH FROM PRIORITY DATE)

No of Legal Status: 006

2/7/15 (Item 1 from file: 351)

009204307 WPI Acc No: 92-331739/40

XRAM Acc No: C92-147538

FLP-mediated gene modification in mammalian cells - giving precise modification by recombination and can be used to alter transgenes for therapeutic purposes and analysis of development

Patent Assignee: (SALK) SALK INST BIOLOGICAL STUDIES

Author (Inventor): OGORMAN S V; WAHL G M

Number of Patents: 001 Number of Countries: 016

Patent Family:

CC Number Kind Date Week

WO 9215694 A1 920917 9240 (Basic)

Priority Data (CC No Date): US 666252 (910308) Applications (CC,No,Date): WO 92US1899 (920306)

Language: English

EP and/or WO Cited Patents: 10Jnl.Ref; US 4959317; US 4997757

Designated States (National): CA; JP

(Regional): AT; BE; CH; DE; DK; ES; FR; GB; GR; IT; LU; MC; NL; SE

Abstract (Basic): WO 9215694 A

Mammalian recombination system (I) comprises:- (a) FLP recombinase or a nucleotide sequence encoding it, and (b) a first DNA comprising a nucleotide sequence contg. up to 1 FLP recombination target site.

Also new are:- (1) a DNA construct comprising as an autonomous fragment, up to 1 FLP recombination target site, up to 1 restriction endonuclease recognition site, up to 1 marker gene, a bacterial origin of replication and opt. a mammalian cellular or viral origin of replication; (2) a DNA construct like that of (1) where the components are contained as an insert in the FLP recombination target site and a 2nd FLP target site is in tandem with the first; (3) assembling of functional gene(s) which is (are) suitable for activation of expression is mammalian cells. The gene segments, derived from up to 1 gene, are individually inactive but contain up to 1 recombination site and are assembled into a functional DNA by contacting with FLP recombinase; (4) disrupting functional gene expression in mammalian cells. Gene of interest contains up to 1 FLP recombination site and is contacted with FLP recombinase and a DNA segment also contg. up to 1 FLP site; (5) the recovery of transfected DNA from the genome of a transfected organism. The DNA contains a fragment with 2 tandemly oriented FLP recombination sites and is contacted with FLP; (6) precisely targeted integration of DNA into the genome of a host organism. An FLP recombination site is introduced into the genome of compatible cells, DNA contg. a recombination site is integrated using FLP recombinase and transformed cells are then introduced into the subject; (7) a mammalian cell contg. up to 1 FLP recombination site in its geromic DNA; (8) a transgenic, non-human mammal contg. up to 1 FLP recombination site in its genome. (9) analysis of the development of a

Salk Institute scientists have shown that the site specific recombinase enzyme, FLP, from Saccharomyces cerevisiae can be used for gene activation in mammalian cells and have suggested it may be useful to mosaically inactivate or activate transgenes or to efficiently integrate transfected DNA at predetermined chromosomal locations.

2/7/13 (Item 1 from file: 315)

328071 CÈABA Accession No.: 24-12-020674 DOCUMENT TYPE: Patent Title: FLP-mediated gene modification in mammalian cells, and compositions and cells useful therefor.

AUTHOR: Wahl, G. M.; O'Gorman, S. V.

CORPORATE SOURCE: Salk Inst. Biol. StudiesLa Jolla, CA 92037USA

CODEN: PIXXD2

PATENT NUMBER: WO 9215694

PUBLICATION DATE: 17 Sep 1992 (920917) LANGUAGE: English PRIORITY PATENT APPLICATION(S) & DATE(S): US 666252 (910308)

ABSTRACT: A gene activation/inactivation and site specific integration system which was developed for mammalian cells is disclosed. The system is based on the recombination of transfected sequences by FLP, a recombinase derived from Saccharomyces. FLP was shown to rapidly and precisely recombine copies of its specific target sequence in several cell lines e.g. a chromosomally integrated, silent .beta.-galactosidase reporter gene was activated for expression by FLP-mediated removal of intervening sequences to generate clones of marked cells whilst, the reverse reaction, is used to target transfected DNA to specific chromosomal sites. FLP can therefore mosaically activate or inactivate transgenes for a variety of therapeutic purposes, as well as for analysis of vertebrate development.

2/7/14 (Item 1 from file: 345) 11153531

Legal Status (No, Type, Date, Code, Text)

WO 9215694 P 910308 WO AA PRIORITY (PATENT)

US 666252 A 910308

WO 9215694 P 920306 WO AE APPLICATION DATA (APPL. DATA) WO 92US1899 A 920306

WO 9215694 P 920917 WO AK DESIGNATED STATES CITED IN A PUBLISHED APPLICATION WITH SEARCH REPORT (DESIGNATED STATES CITED IN A PUBLISHED APPL. WITH SEARCH REPORT)
CA JP

WO 9215694 P 920917 WO AL DESIGNATED COUNTRIES FOR REGIONAL PATENTS CITED IN A PUBLISHED APPLICATION WITH SEARCH REPORT (DESIGNATED COUNTRIES FOR REGIONAL PATENTS CITED IN A PUBLISHED APPL. WITH SEARCH REPORT)

AT BE CH DE DK ES FR GB GR IT LU MC NL SE

WO 9215694 P 920917 WO A1 PUBLICATION OF THE INTERNATIONAL APPLICATION WITH THE INTERNATIONAL SEARCH REPORT (PUB. OF THE INTERNATIONAL APPL. WITH THE INTERNATIONAL SEARCH REPORT)

WO 9215694 P 921223 WO DFPE DEMAND FOR INTERNATIONAL APPLICATION

FILED PRIOR TO EXPIRATION OF 19TH MONTH FROM

mammal comprising:- (a) providing a transgenic mammal comprising:- (i) an expression construct encoding FLP under the control of a condition promoter; and; (ii) a reporter construct under the control of the same or a different promoter. The reporter construct encodes a functional or non-functional gene contg. a recombination site such that functional expression is disrupted or functional expression commences on FLP recombination; and (b) following the development of the mammal to determine when expression of functional reporter gene product either commences or is disrupted; and (10) as co-transfection assay for the occurrence of FLP-mediated recombination in which the expression construct and reporter construct outlined above are contained within plasmids in a mammalian cell.

USE/ADVANTAGE - (I) allows selective modification of chromosomal or extrachromosomal DNA in mammalian cells. Inheritance of genetic sequences and the fate of genetic sequences during development can be studied in a wide variety of tissues in different organisms. Simple histochemical assays can be used for analysis Dwg.0/3B

Derwent Class: B04; C06; D16;

Int Pat Class: C07H-015/12; C12N-005/16; C12N-015/85

2/7/16 (Item 1 from file: 624)

0432248 DIALOG File 624: McGraw-Hill Publications Online

FLP-mediated gene modification in mammalian cells, and compositions and cells useful therefor

Biotechnology Newswatch November 16, 1992; Pg 9; Vol. 12, No. 22

Journal Code: BIO ISSN: 0275-3687

Section Heading: Biotechnology PatentWatch

Word Count: 143

TEXT:

WO 92/15694

Published: Sept. 17, 1992

Filed: March 6, 1992 Priority: March 8, 1991

The Salk Institute For Biological Studies, La Jolla, Ca

A gene activation/inactivation and site-specific integration system has been developed for mammalian cells. The invention system is based on the recombination of transfected sequences by FLP, a recombinase derived from Saccharomyces. In several cell lines, FLP has been shown to rapidly and precisely recombine copies of its specific target sequence. For example, a chromosomally integrated, silent b- galactosidase reporter gene was activated for expression by FLP-mediated removal of intervening sequences to generate clones of marked cells. Alternatively, the reverse reaction can be used to target transfected DNA to specific chromosomal sites. These results demonstrate that FLP can be used, for example, to mosaically activate or inactivate transgenes for a variety of therapeutic purposes, as well as for analysis of vertebrate development.

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Number of sequences searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OI THE INITIAL COMPARISON OF FLP1 (1-34) with:
EMBL-NEW 11, all MAMMALIAN entries
EMBL-NEW 11, all OTHER MAMMALIAN entries
EMBL-NEW 11, all PRIMATE APPRICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        made by low on Tue 1 Feb 94 14:57:16-PST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11, all RODENT entries
79, all MAMMALIAN entries
79, all OTHER MAMMALIAN entries
79, all OTHER VERTEBRATE entries
79, all PATENT entries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIMATE entries
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DENT entries
                                                                                                                                                                                                                                                                                                                                                                                                                     1 OTHER MAMMALIAN entries
1 OTHER VERTEBRATE entries
1 PRIMATE entries
                                                                                                                                                                                                                                                                                                                                                                        entries
                                                                                                                                                                                                                                                                                                                                                                                                           RODENT entries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLP1 (1-34)
112413
4909
                                                                                                                                                                                                                                                                                                       Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
Randomization group
                                                                                                                                                                                                                                                                                                                                                                                                                                     SCORE 0
                                                                                                                   Number of residues:
Number of sequences
Number of scores abo
                                                                                                                                                                                                                                                                    Initial scores to save Optimized scores to save
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100-
f raised to 8.
f raised to 10.
f raised to 11.
f raised to 12.
raised to 13.
raised to 14.
raised to 15.
raised to 15.
                                                                                                                    sequences searched: scores above cutoff:
                                                                                                                                                                    CPU
00:05:58.96
                                                                                                                      cutoff:
                                                                                                                                                                                                                                                                                                                                                                        Unitary
                                                                                                                                                                                                           Mean
8
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                                                                                                                                                                                                                                                                        10
10
                                                                                                                                                                                                                                               SEARCH STATISTICS
                                                                                                                                                                                                                                                                                                                                                                                                 PARAMETERS
                                                                                                                      92888128
112413
4909
                                                                                                                                                                                                                                                                                                                                                                                                                                        215
                                                                                                                                                                                                                                                                                                                                               K-tuple
Joining penalty
Window size
                                                                                                                                                                                                                                                                    Alignments to save Display context
                                                                                                                                                                                                                                                                                                            Number of randomizations
                                                                                                                                                                                                           Median
10
                                                                                                                                                                                                                                                                                                                                                                                                                                        <sup>3</sup> 19 Ξ
                                                                                                                                                                                                           Standard Deviation 4.29
                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 –
                                                                                                                                                                       Total Elapsed 00:11:52.00
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4
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20 to 10 to 1	U 5000-		Data bank : Data bank :	bank :	bank :	Data bank: Data bank: Data bank: Data bank: Data bank:			Query sequence Number of sequence		6. HSFGL2	6. MUSHKPRO	5. Q29100	Sequence Name	The list of other	3. Q12154 4. 2MICRON-B	1. Q25185 2. Q44265	Sequence Name	4 100% similar	The scores belo Significance is	Cut-pff raised to
•		;	VectorBank 6.4 all entries	֓֞֞֞֞֞֞֓֓֓֓֞֞֜֞֡֓֓֓֓֡֡֡֓֡֓֡֓֡֡֡֡֡֡֡֡֡֡֡	RODENT entries all OTHER MAMMALIAN e	GenBank 79, all DYNER MAMMALIAN entries GenBank 79, all OTHER TERTEBRATE entries GenBank 79, all PATENT entries GenBank 79, all PATENT entries GenBank 79, all PRIMATE entries	W 11, all	f the optimized c EMBL-NEW 11, all EMBL-NEW 11, all	Query sequence being compared: FLP1 (1-34) Number of sequences optimized: 4909	1523	Human Fig-2 gene for fibrobla 2887 2 BAIR/c fibroblast growth fact 4158 2	se-keeping protein m 2415	standard deviations above mean of FLP recombination 33	Init. Description Length Score	er best scores is:	Shuttle vector pSW6. B form of the yeast Zmicron p 6248	pSW6 expression vector. 7984 pSW6 for expression of LD78 s 7859	Init. Description Length Score	sequences to the query sequence were found:	The scores below are sorted by initial score. Significance is calculated based on initial score.	to 17.
						٠		:			23 23 23 23		**** 33 33 33 33	. Opt.			34 34 34 34	. Opt.			
										3.27	3.50	3.50	5.83 0	Sig. Frame			6.06	Sig. Frame			
Number of residues: Number of sequences optimized:	Times: CPU 00:01:18.97	Scores: Mean 18	SEAI	Initial scores to save 10 Optimized scores to save 10	Cutoff score 1 Randomization group 1	Similarity matrix Unitary Mismatch penalty 1 Gap penalty 1.00 Gap size penalty 0.33	PARI	STDEV-3 -2 -1 0 SCORE15 16 17 18	-	1 1	1 1	5-1	10-	1 (1) (*	5011	S 100-	1 (P)	ਜ ਹ k	S 500 - *	O O - * *
14160053 4909		Median 20	SEARCH STATISTICS	Alignments to save Display context	Number of	K-tuple Joining penalty Window size	PARAMETERS	1 2 19 20	-										٠	•	
	Total Elapsed 00:04:10.00	Standard Deviation 1.23	Ċ	ntext	Number of randomizations	nalty e		3. 4 21 22	- i							1	*	*		*	
	ed	viation		10 0	s 1	4 30 4		2 5-	-				*								
								25 6	-				•								

The acores below are sorted by optimized score. Significance is calculated based on optimized s based on optimized score.

4 100% similar sequences to the query sequence were found:

Sequence of FLP recombination above mean *** 5. G29100 Sequence of FLP recombination 33 33 12.24 0 **** 5 standard deviations above mean *** 6. RSCALPST Rat mRNA for calpastatin mRNA, comp 1931 18 25 5.71 0 9. HMNSHKPRO 9. HMNSHKPRO 10. G29050 11. FLP1 (1-34) G25185 PSW6 expression vector. 12. G25185 DT 18-NOV-1992 (first entry) DE pSW6 expression vector. Excherichia coli; 2 micron circle; shuttle vector; leu2; EGF; kW ampicilin resistant locus; epidermal growth factor; GAL 1-10; kW ampicilin resistant locus; epidermal growth factor; GAL 1-10; kW ampicilin resistant locus; epidermal growth factor; GAL 1-10; kW ampicilin resistant locus; epidermal growth factor; GAL 1-10; kW applosphoglycerate kinase promoter; PCK; BamHI; HIndIII; ss. Saccharomyces cerevisae PR 23-0CT-1991; GD1860. PR 23-0CT-1991; GD1860. PR 23-0CT-1991; GD1860. PR 23-0CT-1991; GD1860. PR 23-18527/22. PR 29-18527/22. PR 29-18527/22. PR 29-18527/22. PR 29-18527/22. PR 29-18527/22. PR WRI; 32-18527/22. PR WRY; 32-18527/22. PR WRY; 32-18527/22. PR WRY; 32-18527/22. PR New proteins comprising active protein and integrin-affinity promoboils. PS D1sclosure; Page 67; 101pp; English. CC coli as it contains the origin of replication for both organisms. It is a shuttle coli as it contains the origin of replication for both organisms. It is a shuttle coli as it contains the origin of replication for both organisms. It coli and the also contains the leu2 gene (a yeast septential maintenance in Eccoration from thorophesics. CC coli as it contains the sendanced ability for passage through Encoli and CC coli and from the factor and passage through Encoli and CC coli and factorintates genetic manipulation with this vector. pSW6	5185 pSW6 expression vector. 7984 34 4265 pSW6 for expression of LD78 s 7859 34 2154 Shuttle vector pSW6. 7859 34 01CRON-B B form of the yeast 2micron p 6248 34 0f other best scores is: Name Description Length Score	Sequence Name Description Length Score Score Sig. Frame
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7859 BP;

2317 A;

1667 C;

1585 G;

2289 T;

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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Residue Identity
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888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLP1 (1-34)
Q44265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epidermal growth factor (EGF). The expression of the control of an efficient galactose regulated promoter which contains hybrid DNA sequences from the S. cerevisae GAL 1-10 promoter and the S. cerevisae phosphoglycerate kinase (PGK) promoter. Transcription is terminated in this vector by the natural yeast PGK terminator. The EGF gene in pSW6 can be removed by digestion with HindIII and BamBI. This removes DNA encoding both EGF and S amino acids from the C-terminus of the alpha-factor pro-peptide. Genes to be inserted into the pSW6 the alpha-factor pro-peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          044265;
23-NOV-1993 (first entry)
pSW6 for expression of LD78 synthetic gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the alpha-factor pro-peptide. Genes to be inserted into the pSW6 expression vector must therefore have the general composition: HindIII site-alpha-factor adapter-gene-BanHI site.

Sequence 7984 BP; 2348 A; 1698 C; 1635 G; 2303 T;
             The secretion signals from the yeast mating type factor alpha were used to direct export of the LD78 protein. The yeast expression vector pSW6 (NCIMB 40326) is based on the 2 micron circle from S. cerevisiae.
                                                                                                                                                                                      Protein with stem cell inhibition activity, e.g. LD78 or M1P-1 alpha - unable to form stable multimer higher than dodecamer,
                                                                                                            providing better tissue penetration Disclosure; Page 159-168; 294pp; English. An expression vector was designed to enable secretion of LD78 the extracellular medium after expression in S. cerevisiae.
                                                                                                                                                                                                                             WPI; 93-227322/28.
                                                                                                                                                                                                                                               Hunter MG
                                                                                                                                                                                                                                                            23-DEC-1991; GB-027319.
14-OCT-1992; GB-021587.
(BRBI-) BRITISH BIO-TECHNOLOGY LTD.
Craig S, Czaplewski LG, Edwards RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_difference 1773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCI; stem cell inhibition; LD78; ACT2; MIP-lalpha; macrophage inflammatory protein; multimer; tumour therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q44265 standard; DNA; 7859 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contains contains an alpha- factor pre-pro peptide fused in-frame to epidermal growth factor (EGF). The expression of this fusion is under
                                                                                           Secretion aids purification and rapid analysis of LD78.
                                                                                                                                                                                                                                                                                                                                                                                     WO9313206-A.
                                                                                                                                                                                                                                                                                                                                                                                                 note= "base illegible in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   psoriasis; hyperproliferation; yeast expression vector;
                                                                                                                                                                                                                                                                                                                                            23-DEC-1992; G02390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pSW6 for expression of LD78 synthetic gene
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100%
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Optimized Score = 34
Matches = 34
Conservative Substitutions
                                                                                                                                                                                                                                                                      Gilbert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34
34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Significance =
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ti

13.06

, ,:4;

Gaps

Q12154;

Initial Score

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Residue Identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SQ ( 1 Others;
                                                            this fusion is under control of a galactodse regulated promoter this fusion is under control of a galactodse regulated promoter and which contains bybrid DNA from S. cerevisiae GAL 1-10 promoter and the S. cerevisiae phosphoglycerate kinase (PGK) promoter. The EGF gene can be excised by digestion with HindIII and BamHI. The plasmid was used for the expression of a synthetic hirudin HV-1 gene in E. coli K12 HW87. The plasmid can be used to construct expression vectors in which the hirudin gene is linked to a second gene encoding e.g. another hirudin protein, streptokinase or a streptokinase-like protein, via a linking peptide. This peptide link contains a cleavage site for e.g. factor X or thrombin which can be cleaved, releasing the individual proteins which have antitionabotic activity. The enzymes which cleave the fusion protein are present at the site of the target thrombus so the active agents are released specifically at the place where clot formation is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLP1 (1-34)
Q12154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prophylaxis.

Disclosure; Page 71; 115pp; English.

Disclosure; Page 71; 115pp; English.

The vector is based on the 2u circle from S. cerevisiae. It is a deposited in S. cerevisiae strain BJ2168 as NCIMB 40326. It is a shuttle vector capable of replcation in both E. coli and S. cerevisiae and contains origins of replication for both, the leu2 gene (selectable marker), and an ampicillin resistant locus. The E. coli sequences are derived from E. coli ColEI-based replicon pAT153. The vector contains an alpha factor pre-pro-peptide gene fused in frame to the gene for epidermal growth factor (EGF). The expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-DEC-1990; G01911.
07-DEC-1989; GB-027722.
07-DEC-1990; WO-G01911.
 occurring.
See also Q12153-Q12156, Q12158-Q12162 and Q12490.
Sequence 7859 BP; 2317 A; 1656 C; 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dawson KM, Hunter MG, Czapleswski LG;
WPI; 91-208151/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fusion protein; blood clotting; coagulation; fibrinolysis;
antithrombotic; thrombolysis; streptokinase; plasmid; circular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q12154 standard; DNA; 7859 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fusion protein cleavage by blood clotting enzyme - for prodn. fractions having greater antithrombotic activity for therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BRBI-) BRIT BIO-TECHN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-JON-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9109125-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shuttle vector pSW6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7-SEP-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shuttle vector pSW6
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100%
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Substitutions
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34
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Mismatches
                 <u>ڊ</u>
                 2286 T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              = 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Initial
                 Residue Identity
                                                                       FLP1 (1-34)
2MICRON-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGTTCCTATTCTCTAGAAAGTATAGGAACTTC
                                                                                                                                                                                                                                                                                                                                                                                  This is the B form of the yeast 2micron plasmid. Has a single efficient origin of replication that has been localized to a 350bp site lying largely within one inverted repeat. Has two regions of 599bp that are precise inverted repeats of each other. Repeats divide the molecule into approximately equal halves. There are three ORF, two that are necessary to maintain the plasmid in high copy number (REP1 and REP2) and one gene that codes for the FLP protein responsible for the recombination of the molecule in going from the A to B forms using the defined protein regions in the A form in Genbank. Not available commercially. No antibiotic
                                                                                                                                                                                                                                                                                         pept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Broach J.R.;
"The yeast plasmid 2u circle";
Cell 28: 203-204 (1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B form of the yeast 2micron
                                                                       Sequence 6248
                                                                                                                                                                          repeat_unit
                                                                                                                                                                                                                                                     pept
                                                                                                                                          repeat_unit
                                                                                                                                                                                                                                                                                                                                                                       resistance or color markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vector; circular.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IG0001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2MICRON-B
                                                                                                                                                                                                                                                                                                                                                    (SUPPLIER (NONE COMMERCIAL))
                                  Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                    /note="REP1"
4308..5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                       5570..6319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; DNA; 6248 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      n n a
   H (I B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            form of the yeast 2micron plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34
100%
0
34
100%
0
                                                                    /note="2 micron replicon"
BP; 1961 A; 1188 C; 1248 G;
                                                                                                                                               /note="inverted repeat"
3714..4112
                                                                                                                                                                                   341..938
                                                                                                         /note="inverted repeat" 700..1050
                                                                                                                                                                                                                                                                                               3769..2644
                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                /note="FLP"
                                                                                                                                                                                                                                      /note="REP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Optimized Score Matches
                  Optimized Score Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Substitutions
                      n n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 11
                                                                       1851 T; 0 other;
                    34
34
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                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Significance
Mismatches
                                   Significance
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Conservative Substitutions

0 0 0

13.06

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Initial Score = 33
Residue Identity = 100%
Gaps = 0
                                                           rransgenes for therapeutic purposes and analysis of development transgenes for therapeutic purposes and analysis of development Claim 33; Page 40; 49pp; English.

FIP recombinates is a protein which catalyses a site-specific recombination reaction that is involved in amplifying the copy number of the 2-mu plasmid of S. cerevisiae during DNA replication. The inventors claim a mammalian recombination system in which the FIP recombinates is pref. 029101. The FIP recombination target site (FRT) has been identified as minimally comprising two 13 base-pair repeats, separated by an 8 base-pair spacer (see Q29100). The nucleotides in the spacer region can be replaced with any other combination of nucleotides so long as the two 13 base-pair repeats are separated by 8 nucleotides. NB, in the claims the sequence of the FRT has only 12 base pairs on the 3' end of the spacer. The apparently missing base would be C. Sequence 33 BP; 11 A; 5 C; 6 G; 11 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLP1 (1-34)
Q29100
                                                                                                                                                                                                                                                                                          WPI; 92-331739/40.

FLP-mediated gene modification in mammalian cells - giving precise modification by recombination and can be used to alter
                                                                                                                                                                                                                                                                                                                                                 17-SEP-1992.
06-MAR-1992; U01899.
08-MAR-1991; US-666252.
(SALK ) SALK INST BIOLOGICAL STUDIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence of FLP recombination target site FLP recombinase; site-specific integration system; gene activation;
                                                                                                                                                                                                                                                                                                                        Ogorman SV, Wahl GM; WPI; 92-331739/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene inactivation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-1992 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         029100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q29100 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                    NO9215694-
                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                sc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence of FLP recombination target site
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers 14..21
              Optimized Score Matches
                    11 11
               ^{2}_{0}
                 Mismatches
                               Significance
                               11
 12.24
                 Gaps
                               Initial Score
Residue Identity
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STANDARD
FEATURES
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AUTHORS
TITLE
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AUTHORS
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ORGANISM
                                                                              ORIGIN
                                                                                            BASE COUNT
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GAAGGGACTATTC-CTCCAGAGTATAGGAAACTTC X 400 410 420 X
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Ishida, S., Emori, Y. and Suzuki, K.
Rat calpastatin has diverged primary sequence from other realpastatins but retains functionally important sequences Biochim. Biophys. Acta 1088, 436-438 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus sp. Rattus sp. Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae. 1 (bases 1 to 1931)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (12-NOV-1990) Y. Emori, DEPT OF BIOPHYSICS & BIOCHEMISTRY, FACULTY OF SCIENCE, UNIVERSITY OF TOKYO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  calpastatin; CANP inhibitor
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77%
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DALSSDFTCSSPTGKQTEKEKSTGESSKAQSAGVTRSAVPPQEKKRKVEEEVMNDQAL
QALSDSLGTRQPDPQSHLRQAKQVKEAKAKEEERQEKGGEDEDTVPAEYRLKPAKDKOG
KPLLPEPEETSKCLSESELIGELSADFVQPTYQEKPSKPAKIKKGVVPDDAVETLAR
SLGTRKEDPEDEKSIJDKVKEKAKEEDHEKLGEKETIPPDYKLEIVKDKDKRLLPK
                                                                                                                                                                                                                                                                                         IPPEYRHLLDNDGKDKPEKPLDKEHREAGQDQDPIDALSEDLDSCPPTTETSQNTTKEKGKKTSSSKASKNEEKTKDSSKKTEEVPKPKVDEDAT"
                                                                                                                                                                                                                                                                                                                                         EAEEQLPP1SDDF1LDALSQDFSSPANI1S1GFEDAK1SAAVSETVSQVPAPSNHTAA
PPPGTERRDKELDDALDELSDS1GQRQPDPDENKPLDDKVKEKIKAEHSEKLGERDDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MSTTGAKPPVIHEKKPKGKPKEGSETKFQDAPSADGESVAGDVT
VATASDEVVVKKKEKKSLTPTLPMESTLNKLSDKSGVNAALDDLIDTLGECEDTNKDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Rattus sp."
/tissue_type="liver"
/clone_lib="cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="calpastatin/CANP inhibitor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="calpastatin/CANP inhibitor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              evidence=EXPERIMENTAL
                                                                                                                                           Conservative Substitutions
                                                                                                                                                               Optimized Score
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27
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7. FLP1 (1-34) RABCALPA

6

FLP1 (1-34) RSCALPST

Rat mRNA for calpastatin

Conservative Substitutions

Rabbit calpastatin mRNA, complete cds.

RABCALPA 3689 bp ss-mRNA

COS

15-JUN-1989

M

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8. FLP1 (1-34)
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DEFINITION Mouse house-keeping protein mRNA, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS Emori,Y., Kawasaki,H., Imajoh,S., Imahori,K. and Suzuki,K. TTTLE Emori,Y., Kawasaki,H., Imajoh,S., Imahori,K. and Suzuki,K. TTTLE Contains four internal repeats that could be responsible for its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
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                      MUSHKPRO
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                                                              Mouse house-keeping protein mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                 1083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Natl. Acad. Sci. U.S.A. 84, 3590-3594 (1987)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DPEEGKPVADK IKEKSKEEEREKLGEKEETIPPDYRLEEAKDKOGKPLLPSEPTAQLP
ALSEDLILDALSEDF GGPSSASSLKFDDAMLSAAVSEVVSQSPSAS I TRATAPPPDTRP
SNKELDDALDKLSDSLGGRQEPDENKRYMEDKVKERAKKE HKOKLGEBODT IPPEYRH
LLDQGEQDKPEKPPTKKSKE IKKPAGDODP IDALSGDLDSCPPAAETSQATEKDKSKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PQEKKRKVEEDAMSDQALEALSASLGTRMAEPELDLSSIKEVAEAKRKEEKVEKCGED
DETVPAEYRLKPATDKDGKPLLPEPAEKPKPRSESELIDELSKOFSQAKSNEKQPKPT
GKTEESKAAVPAPVAEAVPRTSMCSIQPVPPKPASLQKSTVPDDAVEALAGSLGRKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VDHEKKAQEGKPKEHTKPKSTHKHASDGEGKHGRNEKTASRSKEPVTPAKRTEPETKP
QDTKPAGGKSVAAGTTAAPGKAGDPKKEKKSLPAAALAEPKPDEPSGKSGMDAALDDL
IDTLGEPSETQEDSTAYTGPEISDPMSSTYIEELGKREVTIPPKYRELLEKKTGVAGP
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                                                                                                                                                                                                                                                                                                                                                                                            /organism="Oryctolagus cuniculus"
930 c 943 g 733 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTASSSKAAKHGDKAKDSAQTTEETSKPKANEKNAS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPDSVTPLGPDDAIDALSSDFTCSSPVASGKEAGKEAAKSAGEVLEAESAKVMRAAAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="calpastatin mRNA"
160..428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'codon_start=1
'transTation="MNPAEAKAVPISKEMEGPHPHSKKRHRRQDAKTEPEKSQSTKPP
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'note="calpastatin"
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                        2415 bp 68-mRNA
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                                                                                                                                                                                                                                                                                                              25 Significance
27 Mismatches
                        21-AUG-1991
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ORIGIN
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CDS
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AUTHORS
JOURNAL
STANDARD
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SOURCE
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                                                                                                               TITLE
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                                                                   JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMPC1Q1 3486 bp ss-mRNA PRI 02-NOV-1990 Human plasma cell membrane glycoprotein (PC-1) mRNA, complete M57736 J05654 plasma cell membrane glycoprotein PC-1. Human placenta, cDNA to mRNA, clones lambda-hPC1-2 and lambda-hPC1-3; Human fetal liver, cDNA to mRNA, clones
                                                              Plasma cell membrane glycoprotein PC-1: cDNA cloning of the human molecule, amino acid sequence, and chromosomal location J. Biol. Chem. 265, 17506-17511 (1990)
                                                                                                                                    Buckley, M.F., Loveland, K.A., McKinstry, W.J., Garson, O.M. Goding, J.W.
                                                                                                                                                                          Eukaryota, Animalia, Chordata, Vertebrata, Mammalia, Theria, Eutheria, Primates, Haplorhini, Catarrhini, Hominidae.

1. (bases 1 to 3486)
                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             wang, B., Hunsperger, J.P., Laib, J. and Fan, D.
Unpublished (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
1 (bases 1 to 2415)
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70%
0
    Location/Qualifiers <1..3238
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HLEKSKHGESVNLLKQNLYLVRMTPRRTLFTENLSPLNYDIFFHLVKHCFGKRNAPII
RHLRSLSTVDPINILRQIRKNPGDTAARWYPHDFKKLFETIEQSEDSVFKWIYDYCPE
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PGPGILTGALLKAGARVVAFESEKTFIPHLEPLQRNMDGELQVVHCDFFKMDPRYQEV
VRPDVSSQAIFQNLGIKAVPWSAGVPIKVFGILPYKHERRILWKILFDLYSCESIYRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
478 c 535 g 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="ORF1"
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24 Mismatches
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10
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mRNA

polyA_signal

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/gene="PC1"
3130..3135
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KNIKVIYGPAALTRESDVDRKYSFIVEGIARNLSCREPNGGSCKKYYTYLNKYLGDV
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ADTEENIEVYNLMCDLLNLTPAAPNNGFHGSLNHLLKNPVYTPKHEKEVHPLVQCPFTR
NPRDNLGCSCNPSILPIEDFOTOFNLTVAEEKIIKHETUPYGRPRVLQKENTICLLSQ
HQFMSGYSQDILMPLMTSYTVDRNDSFSTEDFSNGLYQDFRIPLSPVHGCSFYXNNTK
VSYGFLSPPOLNKNSSGIYSBALLTTNIVPMYQSFQVUMRYFHDTLLRKYAEERNGVN
VSYGFLSPPOLNKNSSGIYSBALLTTNIVPMYQSFQVUMRYFHDTLLRKYAEERNGVN
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/transCation="MDVGEEPlekarartak"
/transCation="MDVGEEPlekarartaktool"
/transCation=
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                                                                                                                                 /organism≕"Homo sapiens"
720 c 756 g 988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLFSLDGFRAEYLHTWGGLLPVISKLKKCGTYTKNMRPVYPTKTFPNHYSIVTGLYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="PC1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .64..2785
'gene="PC1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="plasma cell membrane glycoprotein PC-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="PC1"
                                                                                                                                                                                                  Residue
                                                                                                                                                                                                                                          Initial Score
                                                                                                                                                                                                                                                                                                                                             X 10 20 30 X GAAGTTCCTATTCTCTAGAAAGTATAGGAACTT----C
                                                                                                                                                                                                                                                                                                                              plasmid f
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                             production and secretion into the culture medium of human lysozyme. This complete transformation vector is 7850 bpl long and includes the integration vector of the invention and an expression cassette comprising the K. lactis GAL7 promoter, the signal sequence of the K. lactis GAL7 promoter, the signal sequence of the K. lactis killer toxin, the cDNA encoding the ripe form of human lysozyme (HLZ) and the transcription termination signal FLP of the 2 micron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         integrating vector which comprises a region necessary for the stable maintenance of the plasmid in E. coli and a domain which acts as an integrating unit consisting of two not contiguous sequences of the 25 ribosomal DNA from S. cerevisiae, flanking a genetic marker suitable for selection of the yeast transformants in which the integration event has occured. Other DNA sequences may be introduced into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a genetic vector which allows the stable multiple integration of DNA sequences into the genome of Kluyeromyces lactis and Saccharomyces cerevisiae. This sequence can be used in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    integration plasmid, such as expression cassettes. The gene HIS3 from K. lactis and S. cerevisiae is pref. used as a genetic marker for the selection of transformants and an expression cassette for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heterologous proteins
Claim 1; Fig 1; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      which allows stable multiple integration of DNA for prodn. of beterologous proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vector for Kluyeromyces lactis and Saccharomyces cerevisiae
                                                                                                                                                          Score = Identity =
                                                                                                                                                                                                                                                                                                                                                                                     from S.
                                                                                                                                                                                                                                                                                                                                             6824 BP;
                                                                                                                                                19
65%
6
                                                                                                                                                                                                                                                                                                                                                                                          cerevisiae.
                                                                                                                                           Conservative Substitutions
                                                                                                                                                                                        Optimized Score = Matches =
                                                                                                                                                                                                                                                                                                                                        1815 A;
                                                                                                                                                                                                                                                                                                                                        1521 C;
```

255

```
10. FLP1 (1-34)
Q39050
                                                                                                                           Residue Identity
                                                                                                                                       Initial Score
                                              GAATGCTTCCTTTTCACTTAAAAGTAAAGAGAAATTT
860 870 880 890 X
                                                          11 11
K.lactis/S. cerevisae genetic vector
                                                                                                                           16
70%
                                                                                                               Optimized Score = 24
Matches = 26
Conservative Substitutions
                                                                                                                          24 Significano
26 Mismatches
                                                                                                                                        Significance
                                                                                                                                         4
```

2520

GAAGTTCCTATTCTCTAGACAG--CCGGACGGTGGCCA

24 25

Significance = Mismatches =

4.90 7 0

1726 G;

1762

BASE COUNT

1022

source

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AC DIT DE RESERVE PRESERVE PRE
                                                                                                                               21-APR-1993.
31-AUG-1992; 114838.
31-mug-1991; IT-MIZ349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetic; vector; integration; Kluyeromyces lactis; 255 ribosomal DNA; Saccharomyces cerevisiae; E. coli; domain; yeast; plasmid; promoter; expression cassette; HIS3; marker; transformant; human; lysozyme; HIZ; GAL7; signal sequence; killer toxin; transcription termination signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q39050 standard; DNA; 6824 BP. Q39050;
Galeotti CL, Gall
WPI; 93-127394/16.
            K.lactis/S. cerevisae genetic vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JUL-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                          3P-537456-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; signal sequence;
2 micron plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.
                                                               Rossolini GM,
                                                                      Thaller MC;
```

```
Query sequence being compared:
Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                            FastDB - Fast Pairwise Comparison of Sequences Release 5.4
                                                                                                                                                                                                                                                                                                                                                                                          Results file
                                                                                                                                                                                                              Results of the initial comparison of FLP (1-34) with:
a bank : EMBL-NEW 11, all MAMMALIAN entries
a bank : EMBL-NEW 11, all OTHER MAMMALIAN entries
a bank : EMBL-NEW 11, all PRIMATE entries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IntelliGenetics
                                                                                                                                                                                                                                                                                                                                                                                       flp.res\made by low on Tue 1 Feb 94 14:55:48-PST.
                                                                                                                                     MAMMALIAN entries
OTHER MAMMALIAN entries
OTHER VERTEBRATE entries
                                 DENT entries
1 OTHER MAMMALIAN entries
1 OTHER VERTEBRATE entries
1 PRIMATE entries
                                                                                                                                                                                                                                                                                                       FLP (1-34)
112413
3751
PARAMETERS
                                                       15
                                                       3<sup>19</sup>=
```

Cut-off raised to 8. Cut-off raised to 9. Cut-off raised to 11. Cut-off raised to 12. Cut-off raised to 13. Cut-off raised to 14. Cut-off raised to 15. Cut-off raised to 15.	Number of residues: Number of sequences searched: Number of scores above cutoff:	Times: 00	Scores:		Initial scores to save Optimized scores to save	Cutoff score Randomization group	×
	••	CPU 00:05:52.89	Mean 9	SEAR	e 10	1 1 C	Onitary 1 1.00
	92888128 112413 3751		Median 10	SEARCH STATISTICS	Alignments to save Display context	Number of	K-tuple Joining penalty Window size
		Total Elapsed 00:12:19.00	Standard Deviation 4.34	S	to save ntext	Number of randomizations	nalty e
		Ω	iation		0	4ـــر	30 4

1 1 1 1	U 5000-			bank : GenBank-NEW 11, all bank : GenBank-NEW 11, all bank : GenBank-NEW 11, all	bank : GenBank 79, all RODENT entries bank : GenBank NEW 11, all OTHER MAMMALIAN e bank : GenBank-NEW 11, all OTHER TERREPORTER	bank: GenBank 79, all bank: GenBank 79, all bank: GenBank 79, all bank: GenBank 79, all	bank : EMBL-NEW 11, bank : EMBL-NEW 11, bank : EMBL-NEW 11, bank : GenBank 79	timized comparison of FLI	Query sequence being compared: FLP (1-34) Number of sequences optimized: 3751	. MUSMFR3 BALB/c fibroblast growth fac . PIGCA24TA Sus scrofa microsatellite po . SMDEXB S.mutans dextran glucosidase	FGFR3 homolog (mice, bra 2520 Flg-2 gene for fibrobla 2887	5. Q29100 Sequence of FLP recombination 33 33.	Init. Sequence Name Description Length Score	The list of other best scores is:	1. Q25185 pSW6 expression vector. 7984 34 2. Q44265 pSW6 for expression of LD78 s 7859 34 3. Q12154 Shuttle vector pSW6. 7859 34 4. ZMICRON-B B form of the yeast 2micron p 6248 34	Sequence Name Description Length Score	4 100% similar sequences to the query sequence were found:	The scores below are sorted by initial score. Significance is calculated based on initial score.	Cut-pff raised to 17. Cut-bff raised to 18. Cut-off raised to 19.
										26 3.84 0 26 3.62 0 25 3.62 0	26 3.84 26 3.84	* . 33 5.43 0	Opt. Score Sig. Frame		34 5.65 0 34 5.65 0 34 5.65 0 34 5.65 0	Opt. Score Sig. Frame			
Number of residues: Number of sequences	Times:	Scores:		Initial scores to save Optimized scores to sav	Cutoff score Randomization group	Similarity matrix Mismatch penalty Gap penalty Gap size penalty		STDEV-3 -2 -1 SCORE17 18 19	- 1 1 - 1 - 1 - 1 - 1	1 4 1 1	5 -	10-		i (50 -	E O Z :	ਜ਼ ਰ ਨ		F 1000-
optimized:	CPU 00:00:56.90	Mean 20	SEAR	tve 10 save 10	P 1	Unitary 1 1.00 0.33	PARAI	200-								*			*
9352894 3751		Median 21	SEARCH STATISTICS	Alignments to save Display context	Number of r	K-tuple Joining penalty Window size	PARAMETERS	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2											
	Total Elapsed 00:03:35.00	Standard Deviation 1.11		to save text	Number of randomizations	alty		23 24							*	*			
	ea.	viation		0	y	30 4		5 6 25 25											

The scores below are sorted by optimized score. Significance is calculated based on optimized score.

100% similar sequences to the query sequence were found:

_	12.64	14	Ų.		micron p	B form of the yeast 2micron p	4. 2MICRON-B
0	12.64	. u	34	7859		Shuttle vector pSW6.	3. Q12154
0	12.64	34	34	7859	f LD78 s	psw6 for expression o	2. Q44265
0	12.64	34	34		Ħ.	psW6 expression vecto	1. 025185
rame	Init. Opt. Length Score Score Sig. Frame	Opt. Score	Init. Score	Length		Description	Sequence Name

Sequence Name	Description Le	Init. Opt. Length Score Score Sig. Frame	Init. Opt. Score Score	ore	Sig. F	rame
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	**** 11 standard deviations above mean ****	ove mean	* * * * * * * * * * * * * * * * * * * *			
5. Q29100	Sequence of FLP recombination 33 33	ω	ယ	ယ္ထ	11.73 0	0
	**** 6 standard deviations above mean ****	ove mean	* * *			
RSCALPST	Rat mRNA for calpastatin	1931 22	22	27	6.32 0	0
	**** 5 standard deviations above mean ****	ove mean	* * *			
7. HSFGL2	Human Flg-2 gene for fibrobla	2887	26	26	5.42	0
8. MUSMFR3		4158	26	26	5.42	0
PIGCA24TA	Sus scrofa microsatellite pol	211	25	26	5.42	0
10. RABCALPA	٠	3689	25	26	5.42	0

FLP (1-34) Q25185 pSW6 expression vector

```
Escherichia coli; 2 micron circle; shuttle vector; leu2; EGF; ampicilin resistant locus; epidermal growth factor; GAL 1-10; phosphoglycerate kinase promoter; PGK; BamHI; HindIII; ss.
                                                                                                                                                  WO9207874-A
                                                                                                                                                                                           psw6 expression vector.
                                                                                                                                                                                                              Q25185;
                                                                                                                                                                                                                     Q25185 standard; DNA; 7984 BP
                                                                                                                                                          Saccharomyces cerevisae.
                                                                                                                                                                                                   8-NOV-1992 (first entry)
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23-OCT-1991; G01860. 24-OCT-1990; GB-023149. (BRBI-) BRITISH BIO-TECHNOLOGY LTD. Dawson KM, Edwards RM, Fallon A;

New proteins comprising active protein and integrin-affinity sequence - are antithrombotics useful in treating and preventing myocardial infarction, stroke, pulmonary embolism and deep vein WPI; 92-183627/22.

Chrombos18

The sequence given is the yeast expression vector pSW6. It is based on the 2 micron circle from Saccharomyces cerevisae. It is a shuttle vector capable of replication in both S. cerevisae and Escherichia coli as it contains the origin of replication for both organisms. It also contains the leu2 gene (a yeast selectable marker) and the amipicillin resistant locus for selection of plasmid maintenance in E. Disclosure; Page 67; 101pp; English.

> cerevisae phosphoglycerate kinase (PGK) promoter. Transcription is terminated in this vector by the natural yeast PGK terminator. The EGF gene in pSW6 can be removed by digestion with HindIII and BamHI. This removes DNA encoding both EGF and 5 amino acids from the C-terminus of the alpha-factor pro-peptide. Genes to be inserted into the pSW6 expression vector must therefore have the general composition: HindIII site-alpha-factor adapter-gene-BamHI site. this greatly facilitates genetic manipulation with this vector. pSW6 contains contains an alpha- factor pre-pro peptide fused in-frame to epidermal growth factor (EGF). The expression of this fusion is under the control of an efficient galactose regulated promoter which contains hybrid DNA sequences from the S. cerevisae GAL 1-10 promoter and the S. cerevisae phosphoglycerate kinase (PGK) promoter. Transcription is Sequence This vector has enhanced ability for passage through E.coli and 7984 BP; 2348 A; 1698 C; 1636 G; 2303 T;

Residue Initial

34 76% 0

Matches Optimized Score

Conservative Substitutions

Ħ

34 26

Mismatches Significance =

12.64 8 0

Score Identity =

FLP (1-34) Q44265 Q44265 standard; DNA; 7859 Q44265; 23-NOV-1993 (first entry) pSW6 for expression of LD78 synthetic gene. 먥

Location/Qualifiers misc_difference 1773 pSW6 for expression of LD78 synthetic gene.
SCI; stem cell inhibition; LD78; ACT2; MIP-lalpha;
macrophage inflammatory protein; multimer; tumour therapy;
psoriasis; hyperproliferation; yeast expression vector; /*tag= a /note= "base illegible cırcular; ds. accharomyces cerevisiae.

08-UL-1993. 08-UL-1993. 23-DEC-1992; G02390. 23-DEC-1991; GB-027319. 14-OCT-1992; GB-021587. 14-OCT-1992; GB-021587. (BRBI-) BRITISH BIO-TECHNOLOGY LTD. WO9313206-A. in the specification"

Protein with stem cell inhibition activity, e.g. LD78 or MlP-1 alpha - unable to form stable multimer higher than dodecamer, MPI; 93-227322/28.

Gilbert RJ;

Hunter MG;

providing better tissue penetration Disclosure; Page 159-168; 294pp; English.

An expression vector was designed to enable secretion of LD78 to the extracellular medium after expression in S. cerevisiae. Secretion aids purification and rapid analysis of LD78. The secretion signals from the yeast mating type factor alpha were used to direct export of the LD78 protein. The yeast expression

vector pSW6 (NCIMB 40326) is based on the 2 micron circle from

```
Gaps
                                                        Residue Identity
                                                                Initial Score
                                                                                SS CC
       GAAGTTCCTATTCTCTAGAAAGTATAGGAACTT
                       GAAGTTCCTATTCNNNNNNNNGTATAGGAACTTC
                                                                                           S. cerevisiae.
Sequence 7859
                                                                                         Sequence
                                                                                 Others;
3140
                                                  u n
                                                                H
                                                                                           B₽;
                                                         Optimized Score Matches
                                                 Conservative Substitutions
                                                                                           2317
3160
                                30
                                                                                          ?
                                                                                           1667
                                                           8 0
                                                                                           Ç
                                                         34
26
                                                                                           1585 G;
                                                         Mismatches
                                                                Significance =
                                                                                           2289
                                                   ii ii
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12.64 8 0

DAGE STATE OF STATE O , FLP (1-34) Q12154 07-DEC-1990; G01911. 07-DEC-1989; GB-027722. 07-DEC-1990; WO-G01911. (BRBI-) BRIT BIO-TECHN LTD. Q12154 standard; DNA; 7859 BP Q12154; Fusion protein; blood clotting; coagulation; fibrinolysis; antithrombotic; thrombolysis; streptokinase; plasmid; circ Shuttle vector pSW6 Dawson KM, Hunter MG, Czapleswski LG; WO9109125-A. Shuttle vector pSW6 (first entry) circular; ss.

Fusion protein cleavage by blood clotting enzyme – for prodn. fractions having greater antithrombotic activity for therapy of

pisciosure; Page 71; 115pp; English.

The vector is based on the 2u circle from S. cerevisiae. It is deposited in S. cerevisiae strain BM2168 as NCIMB 40326. It is a shuttle vector capable of replication in both E. coli and S. cerevisiae and contains origins of replication for both, the leu2 gene (selectable marker), and an ampicillin resistant locus. The E. coli sequences are derived from E. coli colE1-based replicon pAT153. The vector contains an alpha factor pre-pro-peptide gene fused in frame to the gene for epidermal growth factor (EGF). The expression of this fusion is under control of a galactodse regulated promoter which contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1-10 promoter and the contains hybrid DNA from S. cerevisiae GAI 1 in E. coli K12 HW87. The plasmid can be used to construct expression vectors in which the hirudin gene is linked to a second gene encoding e.g. another hirudin protein, streptokinase or a streptokinase-like protein, via a linking peptide. This peptide link contains a cleavage site for e.g. factor X or thrombin which can be cleaved, releasing the individual proteins which have antithrombotic activity. The enzymes which cleave the fusion protein are present at the site of the target thrombus so the active agents are released specifically at the place where clot formation is occurring. See also Q12153-Q12156, the S. cerevisiae phosphoglycerate kinase (PGK) promoter. The EGF gene can be excised by digestion with HindIII and BamHI. The plasmid was used for the expression of a synthetic hirudin HV-1 gene 12 HW87. The plasmid can be used to construct ex-Q12158-Q12162 and Q12490

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Gaps
                                                                                                                                                                                                                                                                                                          Residue Identity = Gaps =
Initial Score
                                                                                                                                                                                                                                                                                                                                SS
                                                                                                                                                                                                                                                  FLP (1-34)
2MICRON-B
                                                                                                                                                                                                                                                                        GAAGTTCCTATTCTCTAGAAAGTATAGGAACTTC X 3140 3150 3160 X
                                                                                                                                                                                                                                                                                    GAAGTTCCTATTCNNNNNNNGTATAGGAACTTC
                                                                                                                                                                                                      B form of the yeast 2micron plasmid
                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                           Broach J.R.;
                                                                                                                                                                                                                                       2MICRON-B
                                                                                                                                                                                           Vector; circular.
                                                                                                                                                                                                                            IG0001;
                                                                                                                                                                yeast plasmid 2u circle"; 28: 203-204 (1982).
                                                                                                                                                                                                                                                   W
                                                                                                                                                                                                                                       standard; DNA; 6248 BP
                                                                                                                                                                                                                                                                                                                    11
                                                                                                                                                                                                                                                                                                                                7859
                                                                                                                                                                                                                                                  form of the yeast 2micron plasmid
                                                                                                                                                                                                                                                                                                         34
76%
0
                                                                                                                                                                                                                                                                                                                                B₽;
                                                                                                                                                                                                                                                                                                         Conservative Substitutions
                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                    Optimized Score
                                                                                                                                                                                                                                                                                                                                2317
                                                                                                                                                                                                                                                                                               မ
                                                                                                                                                                                                                                                                                                                                A.
                                                                                                                                                                                                                                                                                                                                1656 C;
                                                                                                                                                                                                                                                                                                                    II.
                                                                                                                                                                                                                                                                                                                34
26
                                                                                                                                                                                                                                                                                                                                1600
                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                    Significance =
                                                                                                                                                                                                                                                                                                                                G;
                                                                                                                                                                                                                                                                                                                                2286
                                                                                                                                                                                                                                                                                                                                Į,
                                                                                                                                                                                                                                                                                                                     12.
                                                                                                                                                                                                                                                                                                                     . 64
```

Initial Score pept pept This is the B form of the yeast 2micron plasmid. Has a single efficient origin of replication that has been localized to a 350bp site lying largely within one inverted repeat. Has two regions of 599bp that are precise inverted repeats of each other. Repeats divide the molecule into approximately equal halves. There are three ORF, two that Sequence orgrpl are necessary to maintain the plasmid in high copy number (REP1 and REP2) and one gene that codes for the FLP protein responsible for the recombination of the molecule in going from the A to B forms using the defined protein regions in the A form in Genbank. Not available commercially. No antibiotic repeat_unit repeat_unit resistance or color markers. /note="2 micron replicon" 6248 BP; 1961 A; 1188 C; 1248 G; /note="REP1" 4308..5197 (NONE 5570..6319 II COMMERCIAL)) ű 3714..4112 /note="inverted repeat"
700..1050 /note="inverted repeat" Location/Qualifiers 'note="FLP" note="REP2" Optimized Score ŧI 1851 T; 0 other; 34 Significance = 12.64

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Residue Identity = Gaps =
                                                                                                                                                                 Residue Identity
                                                                                                                                                                                   Initial
                                                                                                                                                                                                                    FIP-mediated gene modification in mammalian cells - giving precise modification by recombination and can be used to alter transgenes for therapeutic purposes and analysis of development Sclaim 33; Page 40; 49pp; English.

FIP recombinates is a protein which catalyses a site-specific recombination reaction that is involved in amplifying the copy number of the 2-mu plasmid of S. cerevisiae during DNA replication. The inventors claim a mammalian recombination system in which the FIP recombinase is pref. 029101. The FIP recombination target site (FRT) has been identified as minimally comprising two 13 base-pair repeats, separated by an 8 base-pair spacer (see 029100). The nucleotides in the spacer region can be replaced with any other combination of nucleotides so long as the two 13 base-pair repeats are separated by 8 nucleotides. NB, in the claims the sequence of the FRT has only 12 base pairs on the 3' end of the spacer. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLP (1-34)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q29100
                                                                      GAAGTTCCTATTCNNNNNNNGTATAGGAACTT
                                               GAAGTTCCTATTCTCTAGAAAGTATAGGAACTT
X 10 20 30 X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-SEP-1992.
06-MAR-1992; U01899.
08-MAR-1991; US-666252.
08-MAR-1991; US-666252.
(SALK ) SALK INST BIOLOGICAL STUDIES OGOTMAN SV, WAN1 GM;
WPI; 92-331739/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence of FLP recombination target site FLP recombinase; site-specific integration system; gene gene inactivation; as.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q29100 standard; DNA; Q29100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                    apparently missing base would be C. Sequence 33 \text{ BP}_i 11 \text{ A}_i 5 \text{ C}_i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  м09215694-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-FEB-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                label= spacer
                                                                                                                                                     H H H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence of FLP recombination target site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                   33
75%
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 14..21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76%
0
                                                                                                                                                Optimized Score = 33
Matches = 25
Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                      11 T;
                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                   Significance
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FLP (1-34)
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STANDARD
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Rat calpastatin has diverged primary sequence from other mammalian calpastatins but retains functionally important sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (12-NOV-1990) Y. Emori, BIOCHEMISTRY, FACULTY OF SCIENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus sp.
Eukaryota; Animalia; Metazoa
Theria; Eutheria; Rodentia;
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IPPEYRHLLDNDGKDKPEKPLDKEHREAGQDQDPIDALSEDLDSCPPTTETSQNTTKE
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KPLLPEDFETSKCLSESELIGELSADFVQPT'QEKESAMPAAKIKKGVVPDDAVETIAR
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PPYTGPVVLDPMDSTYLEALGIKEGTIPPEYRKLLEKNEAITGPLPDSPKPMGIDHAI
DALSSDFTCSSPTGKQTEKEKSTGESSKAQSAGVTRSAVPPQEKKRKVEEEVMNDQAL
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/tissue type="liver"
/clone lib="cDNA"
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cheria; Rodentia; Myomorpha; Muridae; Murinae.
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UNIVERSITY OF TOKYO, 7-3-1 HONGO,
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6. FLP (1-34)

Human Flg-2 gene for fibroblast growth factor rece

Initial Score Residue Identity Gaps	BASE COUNT	CDS	mat_peptide	III NAN		JOURNAL STANDARD FEATURES BOUICE	STANDARD REFERENCE AUTHORS TITLE	REFERENCE AUTHORS TITLE JOURNAL	X	LOGIS DEFINITION ACCESSION KEYWORDS
city =	592		otide			Oncogene 6, 10 full automatic Locat 128	76100 Rehovot, full automatic 2 (bases 1 to Avivi, A., Zimm F1g-2, a new m	1 (base Givol,D. Direct S	human Homo sapiens Eukaryota; A Theria; Euth	HSFGL2 Human F1g-2 X58255 fibroblast
26 Optimized Score = 26 Significance = 5.42 58% Matches = 20 Mismatches = 14 0 Conservative Substitutions = 0	/product="fibroblast growth factor receptor" /product="fibroblast growth factor receptor" /codon start=1 /codon	<pre>/gene="Fig-2" /product="fibroblast growth factor receptor" 2132615 /reconstant</pre>	/note="fibroblast growth factor receptor" 2732612	/gene="F1g-2" /gene=EXPERIMENTAL /evidence=EXPERIMENTAL	<pre>/organism="Homo sapiens" /tissue_type="skin" /cell_type="skinocytes" /tissue_lib="keratinocyte cDNA" 1 2887</pre>	e 6, 1089-1092 (1991) tomatic Location/Qualifiers 1.2887	ehovot, Israel tomatic es I to 2887) ., Zimmer,Y., Yayon,A., Yarden,Y. and Givol,D, a new member of the family of fibroblast growth factor	1 (bases 1 to 2887) Givol, D. Direct Submission Submitted (20-FEB-1991) D. Givol, Weizmann Institute of Science	nimali eria;	HSFGL2 2887 bp RNA PRI 14-AUG-1991 Human Flg-2 gene for fibroblast growth factor receptor XS8255 fibroblast growth factor receptor; Flg-2 gene.
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Initial Score Residue Ident Gaps X 1	source BASE COUNT		CDS	FEATURES sig_peptide	AUTHORS TITLE JOURNAL STANDARD	ORGANISM REFERENCE	KEYWORDS SOURCE	LOCUS DEFINITION	. FLP (1-34) MUSMFR3	X 10 GAAGTTCCTATTC GAAGGTCCTGTTX X 1540
Score = 26 Optimized Score = 26 Significance = 5.42 Identity = 58% Matches = 20 Mismatches = 14 = 0 Conservative Substitutions = 0 10 20 30 X	910 a ~ l de l'k d' l' l' A d' N d' G E	/gene= m.n/ /product="fibroblast growth factor receptor 3" /codon start=1 /transTation="MVVPACVLVFCVAVVAGATSEPPGPEQRVVRRAAEVPGPEPSQQ	/codon_start=1 2272632 //cone="mpqq"		Ornitz,D.M. and Leder,P. Drnitz,D.M. and Leder,P. Ligand specificity and heparin dependence of fibroblast growth factor receptors 1 and 3 J. Biol. Chem. 267, 16305-16311 (1992) full automatic	1 25 2 2	fibroblast growth factor receptor 3; transmembrane protein; fibroblast growth factor receptor 3; transmembrane protein; tyrosine kinase. Mus musculus (strain BALB/c, sub species domesticus) (library: Balb/C brain cDNA library in Lamda ZAP, Stratagene, La Jolla, CA) brain cDNA to mRNA.	MUSMFR3 4158 bp ss-mRNA ROD 03-SEP-1992 BALB/c fibroblast growth factor receptor 3 (mFR3) mRNA, complete cds.) BALB/c fibroblast growth factor receptor 3 (mFR3)	X GAAGTTCCTATTCNNNNNNGTATAGGAACTTC

10. FLP (1-34) RABCALPA REFERENCE AUTHORS DEFINITION ACCESSION KEYWORDS TITLE ORGANISM STANDARD JOURNAL calcium-dependent cysteine protease; calpastatin. Rabbit lung or heart, cDNA to mRNA, clones lambda-Cl-[2,311,11,21,213,413,408]. Oryctolagus cuniculus Rabbit calpastatin mRNA, complete cds. M16476Emori,Y., Kawasaki,H., Imajoh,S., Imahori,K. and Suzuki,K. Endogenous inhibitor for calcium-dependent cysteine protease contains four internal repeats that could be responsible for its multiple reactive sites RABCALPA full automatic Eutheria; Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; (bases 1 to 3689) Rabbit calpastatin mRNA, complete cds. Natl. Acad. Sci. U.S.A. 84, Location/Qualifiers Lagomorpha; Leporidae. 3689 bp ss-mRNA 3590-3594 (1987) MAM 15-JUN-1989

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The acores below are sorted by optimized score. Significance is calculated based on optimized score.

A 100% similar sequence ç the query sequence was found:

10. RATQLIKEB	9 BATCOMIACS	8. HUMC4BAA	DOGRAB5A		6. MUSHKPRO		5. Q29100		4. Q25185	3. Q12154	2. Q44265		Sequence Name		The list of other best scores is:	1. 2MICRON-B	Sequence Name
Rattus norvegicus Q-like gene	Rat carcinoembryonic antigen-	Human complement component C4	C.familiaris GTP-binding prot	**** 4 standard deviations above mean	Mouse house-keeping protein m 2415	**** 5 standard deviations above mean ****	Sequence of FLP recombination	**** 8 standard deviations above mean ****	pSW6 expression vector.	Shuttle vector pSW6.	pSW6 for expression of LD78 s	**** 9 standard deviations above mean ****	Description		best scores is:	B form of the yeast 2micron p 6248	Description
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FLP' (1-34) 2MICRON-B B form of the yeast 2micron plasmid.

IG0001; 2MICRON-B standard; DNA; 6248 BP

B form of the yeast 2micron plasmid

09-SEP-1986

Vector; circular.

Broach J.R.;
"The yeast plasmid 2u circle";
Cell 28: 203-204 (1982).

approximately equal halves. There are three ORF, two that approximately equal halves. There are three ORF, two that approximately equal halves. There are three ORF, two that are necessary to maintain the plasmid in high copy number (REP1 and REP2) and one gene that codes for the FLP protein (REP1 and REP2) and one gene that codes for the FLP protein responsible for the recombination of the molecule in going from the A to B forms using the defined protein regions in the from the A to B forms variable commercially. No antibiotic This is the B form of the yeast 2micron plasmid. Has a single efficient origin of replication that has been localized to a 350bp site lying largely within one inverted repeat. Has two regions of 599bp that are precise inverted repeats of each other. Repeats divide the molecule into approximately equal halves. There are three ORF, two that

> Residue Identity = Gaps = = 30 X
> GAAGTTCCTATACNNNNNNNGAATAGGAACTTC pept pept /note="2 micron replicon" Sequence 6248 BP; 1961 A; 1188 C; 1248 G; pept repeat_unit repeat_unit resistance or color markers. (SUPPLIER (NONE COMMERCIAL)) Score /note="REP2" 5570..6319 /note="REP1" 4308..5197 3714..4112 /note="inverted repeat"
> 700..1050 3769..2644 Location/Qualifiers /note="inverted repeat" 'note="FLP" Optimized Score Matches Conservative Substitutions 0 0 1851 34 26 Mismatches T; 0 other; Significance 11 11.75 8 0

GAAGTTCCTATACTTTCTAGAGAATAGGAACTTC

FLP' (1-34) Q44265 044265 standard; DNA; 7859 BP. 044265; 23-NOV-1993 (first entry) pSW6 for expression of LD78 synthetic gene.

pSW6 for expression of LD78 synthetic gene. SCI; stem cell inhibition; LD78, kCT2; MIP-lalpha; SCI; stem cell inhibition; LD78, kCT2; MIP-lalpha; macrophage inflammatory protein; multimer; tumour therapy; psoriasis; hyperproliferation; yeast expression vector;

psoriasis; hy circular; ds. Saccharomyces cerevisiae. location/Qualifiers

misc difference 1773

/note= "base illegible in the specification" WO9313206-A.

08-JUL-1993. 23-DEC-1992; G02390. 23-DEC-1991; GB-027319. 23-DECT-1992; GB-021587. 14-OCT-1992; GB-021587. (BRBI-) BRITISH BIO-TECHNOLOGY LTD. Craig 5, Czaplewski LG, Edwards R

Hunter MG; WPI; 93-227322/28. Edwards RM, Gilbert RJ;

providing better tissue penetration Disclosure; Page 159-168; 294pp; Eng Protein with stem cell inhibition activity, e.g. LD78 or MIP-1 alpha - unable to form stable multimer higher than dodecamer, 294pp; English.

An expression vector was designed to enable secretion of LD78 to the extracellular medium after expression in S. cerevisiae.

Secretion aids purification and rapid analysis of LD78.

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EO.

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Residue
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. FLP' (1-34)
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GAAGTTCCTATACNNNNNNNNNAATAGGAACTTC
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                                                                                                                                                                           S. cerevisiae
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Shuttle vector pSW6
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Disclosure; Page 11; 115pp; English.

C desposited in S. cerevisiae strain B2168 as NCHMS 40326. It is a coposited in Suntains origins of replication in both E. coli capable vector pswe.

C visiae and contains an alpha factor pre-pro-peptide gene fuse for the sequences are derived from Fulls (selected which contains in whord ydigestion with Hindili and be used for the expression of a synthetic relike protein a cleavage site for e.g. factor and be vector in E. contains a phosphoglyceate kinase (REDI- Dameon REDI B) 1.28 and a supplication in both E. coli micro protein cleavage by blood clotting enzyme - for prodn. of PT Fusion protein cleavage by blood clotting enzyme - for prodn. of PT Fusion protein cleavage by blood clotting enzyme - for prodn. of PT Fusion protein cleavage by blood clotting enzyme - for prodn. of PT Fusion protein cleavage by blood clotting enzyme - for prodn. of PT Fusion protein creable of replication from S. cerevisiae. It is a caposited in S. cerevisiae strain B2168 as NCHMS 40326. It is a caposited in S. cerevisiae of replication for both, the leu2 gene C wisiae and contains origins of replication for both, the leu2 gene C visiae and contains origins of replication for both, the leu2 gene C visiae and contains an alpha factor pre-pro-peptide gene fused in frame C which contains a hybrid DNA from S. cerevisiae GAI 1-10 pyomoter and C streptokinae excised by digestion with Hindill and Bamil. The plasmid can be used to construct excepts and the protein, via a linking peptide. This peptide C link contains a cleavage site for e.g. factor x or thrombin which C can be cleaved, releasing the individual proteins which have anti- C can be cleaved, releasing the individual proteins which have anti- C can be cleaved, releasing the individual proteins which have anti- C can be cleaved, releasing the individual proteins which c can be excised by disease which cleave the fusion protein with agents.
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Initial Score

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Optimized Score =

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Significance =

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See also Q
Sequence
cerevisae phosphoglycerate kinase (PGK) promoter. Transcription is terminated in this vector by the natural yeast terminator. The EGF gene in pSM6 can be removed by digestion with HindIII and BamHI. This removes DNA encoding both EGF and 5 amino acids from the C-terminus of the alpha-factor pro-peptide. Genes to be inserted into the pSM6 expression vector must therefore have the general composition: HindIII site-alpha-factor adapter-gene-BamHI site.

Sequence 7984 BP; 2348 A; 1698 C; 1635 G; 2303 T;
                                                                                                                                                                                               coli as it contains the origin of replication for both organisms. It also contains the leu2 gene (a yeast selectable marker) and the amipicillin resistant locus for selection of plasmid maintenance in E. coli. This vector has enhanced abbility for passage through E.coli and this greatly facilitates genetic manipulation with this vector. pSM6 contains contains an alpha-factor pre-pro peptide fused in-frame to epidermal growth factor (EGF). The expression of this fusion is under
                                                                                                                                                                                                                                                                                                                                                                                                                                   New proteins comprising active protein and integrin-affinity sequence - are antithrombotics useful in treating and preven myocardial infarction, stroke, pulmonary embolism and deep v
                                                                                                                                          the control of an efficient galactose regulated promoter which contains hybrid DNA sequences from the S. cerevisae GAL 1-10 promoter and the S. cerevisae phosphoglycerate kinase (PGK) promoter. Transcription is
                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 67; 101pp; English.

The sequence given is the yeast expression vector pSW6. It is based on the 2 micron circle from Saccharomyces cerevisae. It is a shuttle vector capable of replication in both S. cerevisae and Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-OCT-1991; G01860.
24-OCT-1990; GB-023149.
(BRBI-) BRITISH BIO-TECHNOLOGY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli; 2 micron circle; shuttle vector; leu2; EGF; ampicilin resistant locus; epidermal growth factor; GAL 1-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q25185 standard; DNA; 7984 Q25185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          are released specifically at the place where clot formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dawson KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphoglycerate kinase promoter; PGK; BamHI; HindIII; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pSW6 expression vector.
                                                                                                                                                                                                                                                                                                                                                                                                                    thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09207874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisae
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183627/22.
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7859 BP; 2317 A; 1656 C; 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pSW6 expression vector.
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6. FLP' (1-34)
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                                                                                         GAAGTTCCTATACNNNNNNNNGAATAGGAACTT
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                                                         GAAGTTCCTATTCTCTAGAAAGTATAGGAACTT
X 10 20 30 X
                                                                                                                                                                                                                                                recombination reaction that is involved in amplifying the copy number of the 2-mu plasmid of S. cerevisiae during DNA replication. The inventors claim a mammalian recombination system in which the FLP recombinase is pref. Q29101. The FLP recombination target site (FRT) has been identified as minimally comprising two 13 base-pair repeats, separated by an 8 base-pair ly comprising two 13 base-pair combination of nucleotides so long as the two 13 base-pair repeats are separated by 8 nucleotides. NB, in the claims the sequence of the FRT has only 12 base pairs on the 3' end of the spacer. The apparently missing base would be C. Sequence 33 BP; 11 A; 5 C; 6 G; 11 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAR-1992; U01899.
08-MAR-1991; US-666252.
(SALK ) SALK INST BIOLOGICAL STUDIES.
OGORMAN SV, WAH1 GM;
WPI; 92-331739/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIP-mediated gene modification in mammalian cells - giving precise modification by recombination and can be used to alter transgenes for therapeutic purposes and analysis of development Claim 33; Page 40; 49pp; English.

FIP recombinase is a protein which catalyses a site-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-FEB-1992 (first entry)
Sequence of FLP recombination target site
FLP recombinase, site-specific integration
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Q29100;
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WO9215694-A.
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Canis familiaris
                     Chavrier, P., Parton, R.G., Hauri, H.P., Sim Localization of low molecular weight GTP exocytic and endocytic compartments Cell 62, 317-329 (1990)
                                                                                                                                                                                                C.familiaris
                                                                                                                                                                                                                                          M35520
                                                                                                                                                                                                                                                        C. familiaris GTP-binding protein (rab5) mRNA, complete cds.
     full automatic
                                                                                                                                                                                                                    GTP-binding protein.
                                                                                                                                                                                                                                                                             DOGRAB5A
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                                                                                                                                          Eukaryota;
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/translation="MRGPAMRLPPRLALSALARGPSCILGSGAATRKDWQTRNGRGFS
/translation="MRGPAMRLPPRLALSALARGPSCILGSGAATRKDWQTRNGRGFS
DFNIEDLPDSDLEESSPWTSRNRSEPTRHIACKKAARNLVRDLEEHQNPSRQILLECN
DFNIEDLFGALKAGARVVAFESEKTFIPHLEPLORMBDGELQVVHCDFFKMDPRYQEV
PGPGILTGALLKAGARVVAFESEKTFIPHLEPLORMBGELQVVHCDFFKMDPRYQEV
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478 c 535 g 671
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GRVE LIMEV SEKEFRKLI ATTEKRPD LYQVMAV LIWQVACDVKF LIMEDWSSF SVIMENG
HLEKSKHGESVHLI KQNLJ VURHTERRT LFTENLSP LINYD I FFHLVKHCFSGKUAP I I
RHLRSLSTVDP I NI I LRQI RKNPGDTAARMYPHDFKK LFETI EOSEDSVFKWI YD YCPE
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                                                                                                                       Animalia; Chordata; Vertebrata; Mammalia; Theria;
Carnivora; Caniformia; Canoidea; Canidae.
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21
                                                           Simons, K. and Zerial, TP binding proteins t
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Residue Initial

	/gene="C4BPB" //note="C4b-binding protein beta-chain" sig_peptide 2979 /gene="C4BPB" /gene="C4BPB" /codon start=1 //octe="C4BPB" /cotes" /notes" /notes" /notes"	d sequence for [1] kir	REFERENCE 1 (bases 1 to 848) AUTHORS Hillarp, A. and Dahlback, B. TITLE Cloning of cDNA coding for the beta-chain of human complement component C4b-binding protein: Sequence homology with the alpha chain. Proc. Natl. Acad. Sci. U.S.A. 87, 1183-1187 (1990)	848 bp ss-mRNA PRI 15- lement component C4b-binding protein beta-c lette cds. component C4b-binding protein. r, cDNA to mRNA, clones C1 and A8.	8. FLP' (1-34) HUMC4BAA Human complement component C4b-binding protein bet	X 10 20 30 X GAAGTTCCTATACNNNNNNNGAATAGGAACTTC	Initial Score = 26 Optimized Score = 26 Significance = 4.52 Residue Identity = 58% Matches = 20 Mismatches = 14 Gaps = 0 Conservative Substitutions = 0	COODIT SATATE 1 /COODIN STATE 1 //COODIN SATE 1 /	Base-pairs 664 to 711 form a synthetic peptide used to raise antibodies. FEATURES Location/Qualifiers CDS /	COMMENT Draft entry and computer-readable sequence for [Cell (1990) In press] kindly submitted by P.Chavrier, 22-JUN-1990.
Initial Score = 18 Optimized Score = 26 Significance = 4.52 Residue Identity = 60% Matches = 21 Mismatches = 13	PASE COUNT 193 a 255 c 190 g 190 t ORIGIN	D full automatic Draft entry and computer-readable sequence for [1] kindly submit by W.Zimmermann, 02-MAR-1990. Location/Qualifiers on <1828	Eukaryott Eutheria 1 (base Rebstock cDNA and carcinoe J. Biol.	LOCUS RATCGMIAC3 828 bp ds-DNA ROD 15-SEP-1990 DEFINITION Rat carcinoembryonic antigen-related protein (CGMI) gene, intron B. ACCESSION M32478 J05417 KEYWORDS carcinoembryonic antigen-related protein. SEGMENT 3 of 8 SOURCE R.norvegicus (strain Sprague-Dawley) liver DNA, clone lambda-rnGGM1-1. ORGANISM Battus norvegicus	9. FLP' (1-34) RATCGM1AC3 Rat carcinoembryonic antigen-related protein (CGM1	X 10 20 30 X GAAGTTCCTATACNNNNNNGAATAGGAACTTC	Initial Score = 26 Optimized Score = 26 Significance = 4.52 Residue Identity = 58% Matches = 20 Mismatches = 14 Gaps = 0 Conservative Substitutions = 0	/transTation="MFFWCACCIMVAWRVSASDAEHCPELPPVDNSIFVAKEVEGQIL GTYVCIKGYHLVGKKTLFCAASKEWDNTTTECRLGHCPDPVLNNGEFSSSGPVRVSDK ITFMCNDHYILKGSNRSQCLEDHTWAPPFPICKSRDCDPFROHVHGYFEGNNFTLGST ISYYCEDRYYLVGVCQCVDGEWSSALFVCKLIGEAPKPECEKALLAFGESKNLCEA MENFMQQLKESGWTMEELKYSLELKGAELKAKEL" 1.848 /organism="Homo sapiens" BASE COUNT 229 a 174 c 226 g 219 t ORIGIN	/note="gca in clone Cl; no codon at 86 in clone A8" 29787 /gene="C4BPB" /note="C4b-binding protein beta-chain precursor" /codon start=1	<pre>/codon start=1 /note="C4b-binding protein beta-chain" variation 8688 /gene="C4BPB"</pre>

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Initial Score = Residue Identity = =
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Rattus norvegicus
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
1 (bases 1 to 2043)
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Rattus norvegicus Q-like gene sequence.
L16013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic structure and organization of a Q-like gene in the grc-G/C region of the rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rushton, J.J., Misra, D.N., Kunz, H.W., Cortese Hassett, A.L. and Gill, T.J.III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     *Locus =
                                                                                                                                                                                                                                                                                                                                                                                                                                                      full automatic *Locus = RT(2.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus Q-like gene séquence.
                                                                                                                                                                    387
                                                                                                                                                                /haplotype="r21"
/tissue_type="liver"
/sequenced_mol="DNA"
a 558 c 449 g
                                                                                                                                                                                                                                                                                                  R6..91

86..91

/note="this polyadenylation signal was selected because of its similarity to RT1.0; putative"

1013..1264

/note="this 252 nucleotide repeat alters the DNA conformation and is associated with at least one rat MHC class I sequence; putative"

1755..1766

/note="ATGC repeat noted but absent in the RT1.0 gene;
                                                                                          25 Optimized Score58% Matches0 Conservative Sub
                                                                                                                                                                                                                         /organism="Rattus norvegicus"
/dev_stage="adult"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative Substitutions
                                                                                          Conservative Substitutions
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20
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) Mismatches =
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Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Results file flpli.res made by low on Tue 1 Feb 94 15:25:07-PST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FastDB - Fast Pairwise Comparison of Sequences Release 5.4
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                                                                                                                                                        5000-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IntelliGenetics
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11 OTHER MAMMALIAN entries
11 OTHER VERTEBRATE entries
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112413
4804
Cut-off raised to 8.
Cut-off raised to 10.
Cut-off raised to 11.
Cut-off raised to 12.
Cut-off raised to 13.
Cut-off raised to 14.
                                                                                                                                                                                                                                                                                     Gap penalty
Gap size penalty
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Randomization group
                                                                                         Number of residues:
Number of sequences
Number of scores abo
                                                                                                                                                                                                                                                                                                                                       Similarity matrix Mismatch penalty
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Window size
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お田 B M G B S 5000 L I I I I I I I I I I I I I I I I I	Data bank : N Data bank : U Data bank : V	bank :	bank : bank : bank : bank : bank : bank :	equence of sequ esults bank: bank:	6. MUSHKOPRO 7. RABCALPA 8. Q23917 9. DOGRAB5A 10. N82201	2. Q44265 3. Q12154 4. Q25185 5. Q29100	Sequence Name	The list of other	1. 2MICRON-B	Sequence Name	A 100% similar s	Cut-pff raised t The scores below Significance is
	N-GeneSeq 13, all entries UEMBL 36 79, all entries VectorBank 6.4, all entries	all PF all RC 11, al 11, al 11, al		g compared: FI optimized: optimized comparisc e optimized comparisc -NEW 11, all MAMMALIA -NEW 11, all OTHER MA	house-keeping protein m 2415 2 t calpastatin mRNA, comp 3689 2 NA polymerase I coding s 4286 2 iliaris GTP-binding prot 796 2 amylase from plant seed. 1794 2	**** 4 standard deviations above mean **** pSW6 for expression of LD78 s 7859 28 28 4.64 Shuttle vector pSW6. 7859 28 28 4.64 pSW6 expression vector. 7984 28 28 4.64 Sequence of FLP recombination 33 27 27 4.40 **** 3 standard deviations above mean ****	Description Length Score Score Sig. F	best scores is:	B form of the yeast 2micron p 6248 34 34 6.03	Description Length Score Score Sig. Fr	sequence to the query sequence was found:	Cut-pff raised to 17. The scores below are sorted by initial score. Significance is calculated based on initial score.
Times: CPU Total Elapsed 00:01:14.07 00:04:34.00 Number of residues: 13074913 Number of sequences optimized: 4804	SEARCH STATISTICS Scores: Mean Median Standard Deviation 18 20 1.19	Cutoff score Cutoff score Randomization group Initial scores to save Optimized scores to save	PARAMETERS Similarity matrix Unitary K-tuple Mismatch penalty 1 Joining penalty Gap penalty 1.00 Window size 4	O			50- *		0 S 100-	Frame C - *	*	F 1000 - * * * * * * * * * * * * * * * * *

hristopher Lo

The acores below are sorted by optimized score. Significance is calculated based on optimized s score

100% similar sequence to the query sequence was found:

Sequence Name	Description	Init. Opt. Length Score Score Sig. Frame	Init. Opt. Score Scor	Opt. Score	sig. I	rame
1. 2MICRON-B	B form of the yeast 2micron p 6248		34	34 13.47 0	13.47	0
The list of other best scores is:	best scores is:					
Sequence Name	Description	=	Init. Opt. Score Scor	Opt. Score	Sig. F	rame
	**** 8 standard deviations above mean ****	æ	n ***	*		
2. 044265	pSW6 for expression of LD78 s 7859	7859	28		8.42	0
3. Q12154	Shuttle vector psW6.	7859	28	28	8.42	0
4. Q25185	<pre>pSW6 expression vector. 7984 28 **** 7 standard deviations above mean ****</pre>	7984 above mea	n 28	* 28	8.42	0
5. Q29100	Sequence of FLP recombination 33 27 **** 6 standard deviations above mean ****	33 above mea	27 n ***	* 27	7.58	0
6. MUSHKPRO	Mouse house-keeping protein m 2415 25	2415	* 25 * 25	* 26	6.73	0
	**** 5 standard deviations above mean ****	above mea	n ***	*		

FLP1' (1-34) 2MICRON-B

10.

Q23917

Human histone H2A.Z gene, ups 3088
**** 4 standard deviations above m
Taf DNA polymerase I coding s 4286

9.87

OCCASB5 RSCALPST HUMH2AZA

Rat mRNA for calpastatin Rabbit DNA for 5'flanking

reg

19 19 17

224

 $\sigma \sigma \sigma$.05

000

4.21

0

œ form of the yeast 2micron

2MICRON-B standard; DNA; 6248 BP

09-SEP-1986

B form of the yeast 2micron plasmid

Vector; circular.

Broach

The ch J.R.;
yeast plasmid 2u circle";
28: 203-204 (1982).

Cell

This is the B form of the yeast 2micron plasmid. Has a single efficient origin of replication that has been localized to a 350bp site lying largely within one inverted repeat. Has two regions of 599bp that are precise inverted repeats of each other. Repeats divide the molecule into approximately equal halves. There are three ORF, two that are necessary to maintain the plasmid in high copy number (REP1 and REP2) and one gene that codes for the FIP protein responsible for the recombination of the molecule in going from the A to B forms using the defined protein regions in the A form in Genbank. Not available commercially. No antibiotic

> Residue Identity Initial 3860 88888888888888888888888888888888888 Sequence 6248 pept Key repeat_unit repeat_unit resistance or color markers. (SUPPLIER (NONE COMMERCIAL)) Score 3870 /note="REP2" 5570..6319 /note="REP1" 4308..5197 0 0 34 100% 0 /note="2 micron replicon" BP; 1961 A; 1188 C; 1248 G; /note="inverted repeat"
> 3714..4112 /note="inverted repeat" 700..1050 Location/Qualifiers note="FLP" Matches = 34 Conservative Substitutions Optimized Score 3890 1851 $\frac{34}{4}$ Significance Mismatches Τ; 0 other; 13.47

FLP1' Q44265 (1-34)pSW6 for expression of LD78 synthetic gene

Q44265 standard; DNA; 7859 Q44265; BP.

23-NOV-1993 (first entry)

pSW6 for expression of LD78 synthetic gene.
SCI; stem cell inhibition; LD78; ACTZ; MIP-lalpha;
macrophage inflammatory protein; multimer; tumour therapy;

psoriasis; hyperproliferation; yeast expression vector;

circular; ds.

ney Location/Qualifiers misc difference 1773 Saccharomyces cerevisiae

the specification"

08-JUL-1993. WO9313206-A. /*tag= a /note= "base illegible in

23-DEC-1992; G02390. 23-DEC-1991; GB-027319. 23-DECT-1992; GB-021587. 14-OCT-1992; GB-021587. (BRBI-) BRITISH BIO-TECHNOLOGY LTD. Craig S, Czaplewski LG, Edwards RM,

Gilbert

dodecamer,

10

Hunter MG;

Protein with stem cell inhibition activity, e.g. LD78 alpha - unable to form stable multimer higher than doc WPI; 93-227322/28.

providing better tissue penetration Disclosure; Page 159-168; 294pp; English. An expression vector was designed to enable secretion of LD78 the extracellular medium after expression in S. cerevisiae. Secretion aids purification and rapid analysis of LD78.



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clot formation

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Residue
                                                                                                            cc shittle vector capable of replcation in both E. coli and S. cere-
cc visiae and contains origins of replication for both, the leu2 gene
cc (selectable marker), and an ampicillin resistant locus. The E. coli
cs equences are derived from E. coli ColE1-based replicon pATI53. The
cvector contains an alpha factor pre-pro-peptide gene fused in frame
ct to the gene for epidermal growth factor (EGF). The expression of
ct this fusion is under control of a galactodse regulated promoter
ct which contains hybrid DNA from S. cerevisiae GAL 1-10 promoter and
the S. cerevisiae phosphoglycerate kinase (PGK) promoter. The EGF
cc gene can be excised by digestion with HindIII and BamHI. The plas-
cc mid was used for the expression of a synthetic hirudin HV-1 gene
con E. coli K12 HWB7. The plasmid can be used to construct ex-
customer encoding e.g. another hirudin gene is linked to a second
conse encoding e.g. another hirudin profess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLP1'
Q12154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAAGTTCCTATACTTTCTAGAGAATAGGAACTTC
pression vectors in which the natural protein, streptoxings pression vectors in which the natural protein, streptoxings or the protein protein, via a linking peptide. This peptide streptoxinase-like protein, via a linking peptide protein which link contains a cleavage site for e.g. factor X or thrombin which can be cleaved, releasing the individual proteins which have antican be cleaved, releasing the enzymes which cleave the fusion protein can be cleaved, releasing the enzymes which cleave the fusion protein can be cleaved. The enzymes which cleave the fusion protein can be cleaved, releasing the enzymes which cleave the fusion protein can be cleaved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The secretion signals from the yeast mating type factor alpha were used to direct export of the LD78 protein. The yeast expression vector pSW6 (NCIMB 40326) is based on the 2 micron circle from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used to direct export vector pSW6 (NCIMB 403 S. cerevisiae.
                                                                                                                                                                                                                                                                                                                                          The vector is based on the 2u circle from S. cerevisiae deposited in S. cerevisiae strain BJ2168 as NCIMB 40326 shuttle vector capable of repleation in both E. coli and
                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusion protein cleavage by blood clotting enzyme - for prodn. fractions having greater antithrombotic activity for therapy a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusion protein; blood clotting; coagulation; fibrinolysis; antithrombotic; thrombolysis; streptokinase; plasmid; circular; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q12154 standard; DNA; 7859 BP
Q12154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 71; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   prophylaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dawson KM, Hunter MG, Czapleswski LG;
WPI; 91-208151/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-DEC-1990; WO-G01911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-DEC-1990; G01911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9109125-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shuttle vector pSW6
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                    Initial Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pSW6 expression vector.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         See also
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                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 67; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-OCT-1990; GB-023149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09207874-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q25185 standard; DNA; 7984
Q25185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-MAY-1992.
23-OCT-1991; G01860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BRBI-) BRITISH BIO-TECHNOLOGY LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identity
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7859 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pSW6 expression vector
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                                                        7984 BP;
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824
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                    Optimized
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                      Score =
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                                                          1698
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on the 2 micron circle from Saccharomyces cerevisae. It is a shuttle vector capable of replication in both S. cerevisae and Escherichia coli as it contains the origin of replication for both organisms. It also contains the leu2 gene (a yeast selectable marker) and the amipicillin resistant locus for selection of plasmid maintenance in E. coli. This vector has enhanced ability for passage through E.coli and this greatly facilitates genetic manipulation with this vector. pSW6 contains contains an alpha-factor pre-pro peptide fused in-frame to epidermal growth factor (EGF). The expression of this fusion is under the control of an efficient galactose regulated promoter which contains hybrid DNA sequences from the S. cerevisae GAL 1-10 promoter and the S. cerevisae phosphoglycerate kinase (PGK) promoter. Transcription is terminated in this vector by the natural yeast PGK terminator. The EGF gene in pSW6 can be removed by digestion with Hindill and BamHI. This removes DNA encoding both EGF and 5 amino acids from the C-terminus of the alpha-factor pro-peptide. Genes to be inserted into the pSW6 New proteins comprising active protein and integrin-affinity sequence — are antithrombotics useful in treating and preven myocardial infarction, stroke, pulmonary embolism and deep v the alpha-factor pro-peptide. Genes to be inserted into the pSW6 expression vector must therefore have the general composition: HindIII site-alpha-factor adapter-gene-BamHI site. phosphoglycerate kinase promoter; PGK; BamHI; HindIII; ss. Escherichia coli; 2 micron circle; shuttle vector; leu2; EGF; ampicilin resistant locus; epidermal growth factor; GAL 1-10; The sequence given is the yeast expression vector pSW6. Conservative Substitutions Q12158-Q12162 and Q12490. 2317 A; 1656 C; 1600 Ç 28 28 1600 Mismatches Significance ç d preventing deep vein 2286 It is based Η. 8.42 6 0

28

Significance =

8.42

Residue Identity

g n

. FLP1' (Q29100

(1-34)

Q29100;

Synthetic.

sc feature

WO9215694-A.

/label=

spacer

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The inventors claim a mammalian recombination system in which the FIP recombinase is pref. 029101. The FIP recombination target site (FRT) has been identified as minimally comprising two 13 base-pair repeats, separated by an 8 base-pair spacer (see 029100). The nucleotides in the spacer region can be replaced with any other combination of nucleotides so long as the two 13 base-pair repeats are separated by 8 nucleotides. NB, in the claims the sequence of the FRT has only 12 base pairs on the 3' end of the spacer. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLP-mediated gene modification in mammalian cells - giving precise modification by recombination and can be used to alter transgenes for therapeutic purposes and analysis of development claim 33; Page 40; 49pp; English.
FLP recombinase is a protein which catalyses a site-specific recombination reaction that is involved in amplifying the copy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-SEP-1992.
06-MAR-1992; U01899.
06-MAR-1991; US-666252.
08-MAR-1991; US-666252.
(SALK ) SALK INST BIOLOGICAL STUDIES.
OGOTIMAN SV, Wahl GM;
WPI; 92-331739/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-1992 (first entry)
Sequence of FLP recombination target site
FLP recombinase; site-specific integration system; gene activation;
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                                                                                                                                                                                                                                           apparently missing base would be C. Sequence 33 BP; 11 A; 5 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           number of the 2-mu plasmid of S. cerevisiae during DNA replication.
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Submitted (04-JUL-1989) Thomas B., Swiss Federal Institute of Technologie Zuerich, C/O Dr K Buerki Preclinical Research Sandoz Ltd, 4002 Basel , Switzerland.
                                                                                                                                                                    Oryctolagus cuniculus
                                                                                                                                                                                                                            Rabbit DNA for 5'flanking region of beta-casein gene
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                                                                  Direct Submission
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1 (bases 1 to 2157)
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Unpublished (1991)
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//ransIation="MRGPAMRLPPRLALSALARGPSCILGSGAATRKDWQTRNGRGFS
DFNIEPLPDSDLEESSPWTSRNRSEPTRHIACKKAARNILVRDLLEHQNPSRQIILECN
PGPGILTGALLKAGARVVAFESEKTFIPLEPLQRNMDGELQVVHCDFFKMDFRYQEV
PRDPVSSQAIFQNLGIKAVPWSAGVPIKYFGILFYKHERRILMKFVSESTSVHREMG
GRVELLMMFVSEKEFFKLIATPRKSDLYQVMAVLMQVACDVKFLHMEPMSSTSVHREMG
GRVELLMSTVSEKEFFKLIATPRKSDLYQVMAVLMQVACDVKFLHMEPMSSTSVHREMG
HLEKSKHGESVNLLKQNLYLVRMTPRRTLFTENLSPLNYDIFFHLVKHGFGKRNAPII
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478 c 535 g 671
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      2 (bases 1 to 1931)

1 Tahida, S., Emori, Y. and Suzuki, K.

Rat calpastatin has diverged primary sequence from other mammalian calpastatins but retains functionally important sequences

Biochim. Biophys. Acta 1088, 436-438 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 Thomas, B., E Unpublished
                                                                                                                Submitted (12-NOV-1990) Y. Emori, BIOCHEMISTRY, FACULTY OF SCIENCE, BUNKYO-KU, TOKYO 113, JAPAN
                                                                                                                                                                                    Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
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/clone_Tib="lambda-dash"
/chromosome="12q24"
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                                                                                                                                             Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.

1 (bases 1 to 3088)
Hatch, C.L. and Bonner, W.M.
The human histone H2a.z gene: Sequence and regulation
J. Biol. Chem. 265, 15211-15218 (1990)
                                                                                                                                                                                                                                                      Homo sapiens
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L10137 M33917
                                                                                                                                                                                                                                                                     Homo sapiens DNA.
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/sequenced_mol="DNA"
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PPPGTERRDKELDDALDELSDSLGORQPDPDENKPLDDKVKEKIKAEHSEKLGERDDT
IPPEYRHLLDNDGKDKPEKPLDKEHREAGQDQDPIDALSEDLDSCPPTTETSQNTTKE
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DALSSDFTCSSPTGKQTEKEKSTGESSKAQSAGVTRSAVPPQEKKRKVEEEVMNDQAL
QALSDSIGTRQPDPQSHLRQAKQVKEAKAKEEERGEKGEDEDTVPAEYRLKPAKDKD
KPLLPEPEETSKCLSESELIGELSADFVQPTYQEKPSMPAKIKKGVVPDDAVETLAR
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/tissue_type="liver"
/clone_lib="cDNA"
                                                                                                                                 Location/Qualifiers
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/note="calpastatin/CANP inhibitor"
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/translation="MSTTGAKPPVIHEKKPKGKPKEGSETKFQDAPSADGESVAGDVT
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Q23917
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Claim 8; Page 6; 80pp; English.

Chromosomal DNA from Thermosipho africanus (Taf) was PCR-amplified

Chromosomal DNA from Thermosipho africanus (Taf) was PCR-amplified

Cwith degenerate primers corresponding to the amino acid sequences

of conserved regions of known thermostable polymerases. When

specific PCR products of a similar size to the product generated

cusing Tag chromosomal DNA were produced, the PCR fragments were

cloned and sequenced. Fragments with sequences which encoded

regions of amino acid homology to known thermostable polymerases

were identified. The cloned PCR products were used as probes to

screen a genomic Southern blot. The full-length Taf coding sequence

was then compiled from various clones. See also Q23918-Q23961.

Sequence 4286 BP; 1623 A; 470 C; 847 G; 1346 T;
X 10 20 30 X GAAGTTCCTATACTTTCTAGAGAATAGGAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q23917 standard; DNA; 4286 BP.
Q23917;
27-OCT-1992 (first entry)
Taf DNA polymerase I coding sequence.
Thermostability; PCR; polymerase chain reaction;
thermophilic bacteria; Taf Pol I; ss.
                                                                                                                                                                                                                                                                                                                                                                                                              Thermostable DNA polymerase from Thermosipho africanus - prepd.
by purificn. from cells or by expression of Taf polymerase gene
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Abramson RD, Gelfand DH, Greenfield L, Lawyer FC, Reichert FL;
WPI; 92-150887/18.
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28-SEP-1990;
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Set Description Items

SI 346 FLP (10N) RECOMBINAS? **S2** 124 RD (unique items)

?#223/1-124

2/3/1 (Item 1 from file: 155)

08080444 92218444

Reactions between half- and full-FLP recombination target sites. A model system for analyzing early steps in FLP protein-mediated site-specific recombination.

Qian XH; Inman RB; Cox MM

Department of Biochemistry, College of Agricultural and Life Sciences, University of Wisconsin, Madison 53706.

J Biol Chem (UNITED STATES) Apr 15 1992, 267 (11) p7794-805, ISSN 0021-9258 Journal Code: HIV

Contract/Grant No.: GM-32335; GM-14711

Languages: ENGLISH

Document type: JOURNAL ARTICLE

(Item 2 from file: 155) 5%3/5

07913378 92051378

GLP-mediated recombination in the vector mosquito, Aedes aegypti.

Morris AC; Schaub TL; James AA

Department of Molecular Biology & Biochemistry, University of California. Irvine 92717.

Nucleic Acids Res (ENGLAND) Nov 11 1991, 19 (21) p5895-900, ISSN

0305-1048 Journal Code: O&L

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/3 (Item 3 from file: 155)

07823652 91342652

Synapsis, strand scission, and strand exchange induced by the FLP recombinase: analysis with half-FRT sites.

Amin A; Roca H; Luetke K; Sadowski PD

Department of Medical Genetics, University of Toronto, Ontario, Canada.

Mol Cell Riol Sep 1991, 11 (9) p4497-508, ISSN 0270-7306

Journal Code: NGY

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/4 (Item 4 from file: 155)

07777737 91296737

Domain of a yeast site-specific recombinase (Flp) that recognizes its target site.

Chen JW; Evans BR; Yang SH; Teplow DB; Jayaram M

Department of Microbiology, University of Texas, Austin 78712.

Proc Natl Acad Sci U S A Jul 15 1991, 88 (14) p5944-8, ISSN 0027-8424 Journal Code: PV3

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/5 (Item 5 from file: 155)

07731454 91250454

Identification of the DNA-binding domain of the FLP recombinase.

Pan H; Clary D; Sadowski PD

Department of Medical Genetics, University of Toronto, Ontario, Canada.

J Biol Chem Jun 15 1991, 266 (17) p11347-54, ISSN 0021-9258

Journal Code: HIV Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/6 (Item 6 from file: 155)

07687992 91206992

Integration specificity of retrotransposons and retroviruses.

Sandmeyer SB; Hansen LJ; Chalker DL

Department of Microbiology and Molecular Genetics, College of Medicine, University of California, Irvine 92717.

Annu Rev Genet 1990, 24 p491-518, ISSN 0066-4197 Journal Code: 6DP

Contract/Grant No.: GM33281

Languages: ENGLISH

Document type: JOURNAL ARTICLE; REVIEW; REVIEW, ACADEMIC

2/3/7 (Item 7 from file: 155)

07668658 91187658

A bacterial model system for chromosomal targeting.

Huang LC: Wood EA: Cox MM

Department of Biochemistry, College of Agricultural and Life Sciences, University of Wisconsin-Madison 53706.

Nucleic Acids Res Feb 11 1991, 19 (3) p443-8, ISSN 0305-1048

Journal Code: O&L

Contract/Grant No.: GM37835

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/8 (Item 8 from file: 155)

07645850 91164850

Recombinase-mediated gene activation and site-specific integration in mammalian cells.

O'Gorman S; Fox DT; Wahl GM

Gene Expression Laboratory, Salk Institute for Biological Studies, La Jolla, CA 92037.

Science Mar 15 1991, 251 (4999) p1351-5, ISSN 0036-8075

Journal Code: UJ7

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/9 (Item 9 from file: 155)

07643634 91162634

Tyr60 variants of Flp recombinase generate conformationally altered protein-DNA complexes. Differential activity in full-site and half-site recombinations.

Chen JW; Evans BR; Zheng L; Jayaram M

Department of Microbiology, University of Texas at Austin, Austin 78712.

J Mol Biol Mar 5 1991, 218 (1) p107-18, ISSN 0022-2836

Journal Code: J6V

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/10 (Item 10 from file: 155)

07554393 91073393

FLP protein of 2 mu circle plasmid of yeast induces multiple bends in the FLP recognition target site.

Schwartz CJ; Sadowski PD

Department of Medical Genetics, University of Toronto, Ontario, Canada.

J Mol Biol Nov 20 1990, 216 (2) p289-98, ISSN 0022-2836

Journal Code: J6V Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/11 (Item 11 from file: 155)

07553382 91072382

Protein-based asymmetry and protein-protein interactions in FLP recombinase-mediated site-specific recombination.

Qian XH; Inman RB; Cox MM

Program in Cell and Molecular Biology, College of Agricultural and Life Sciences, University of Wisconsin, Madison 53706.

J Biol Chem Dec 15 1990, 265 (35) p21779-88, ISSN 0021-9258

Journal Code: HIV

Contract/Grant No.: GM 37835; GM 14711

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/12 (Item 12 from file: 155)

07490349 91009349

Identification of the active site tyrosine of Flp recombinase. Possible relevance of its location to the mechanism of recombination [published erratum appears in J Biol Chem 1991 Apr 15;266(11):7312]

Evans BR; Chen JW; Parsons RL; Bauer TK; Teplow DB; Jayaram M

Department of Molecular Biology, Research Institute of Scripps Clinic, La Jolla, California 92037.

J Biol Chem Oct 25 1990, 265 (30) p18504-10, ISSN 0021-9258

Journal Code: HIV Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/13 (Item 13 from file: 155)

07410836 90317836

Synaptic intermediates promoted by the FLP recombinase.

Amin AA; Beatty LG; Sadowski PD

Department of Medical Genetics, University of Toronto, Ontario, Canada.

J Mol Biol Jul 5 1990, 214 (1) p55-72, ISSN 0022-2836

Journal Code: J6V

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/14 (Item 14 from file: 155)

07263960 90170960

Functional analysis of Arg-308 mutants of Flp recombinase. Possible role of Arg-308 in coupling substrate binding to catalysis.

Parsons RL; Evans BR; Zheng L; Jayaram M

Research Institute of Scripps Clinic, La Jolla, California 92037.

J Biol Chem Mar 15 1990, 265 (8) p4527-33, ISSN 0021-9258

Journal Code: HIV Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/15 (Item 15 from file: 155)

07229522 90136522

Use of site-specific recombination to regenerate selectable markers.

Cregg JM; Madden KR

Salk Institute Biotechnology/Industrial Associates, Inc., La Jolla, CA 92037.

Mol Gen Genet Oct 1989, 219 (1-2) p320-3, ISSN 0026-8925

Journal Code: NGP

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/16 (Item 16 from file: 155)

07190832 90097832

Characterization of Holliday structures in FLP protein-promoted site-specific recombination.

Meyer-Leon L; Inman RB; Cox MM

Program in Cellular and Molecular Biology, College of Agricultural and Life Sciences, University of Wisconsin-Madison 53706-1569.

Mol Cell Biol Jan 1990, 10 (1) p235-42, ISSN 0270-7306

Journal Code: NGY

Contract/Grant No.: GM37835; GM14711

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/17 (Item 17 from file: 155)

07123422 90030422

The FLP recombinase of yeast catalyzes site-specific recombination in the Drosophila genome.

Golic KG: Lindquist S

Howard Hughes Medical Institute, Department of Molecular Genetics and Cell Biology, University of Chicago, Illinois 60637.

Cell Nov 3 1989, 59 (3) p499-509, ISSN 0092-8674 Journal Code: CQ4 Contract/Grant No.: GM 25874

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/18 (Item 18 from file: 155)

07011744 89313744

Synthesis of an enzymatically active FLP recombinase in vitro: search for a DNA-binding domain.

Amin AA; Sadowski PD

Department of Medical Genetics, University of Toronto, Ontario, Canada.

Mol Cell Biol May 1989, 9 (5) p1987-95, ISSN 0270-7306

Journal Code: NGY

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/19 (Item 19 from file: 155)

07002130 89304130

FLP-FRT mediated intrachromosomal recombination on a tandemly duplicated YEp integrant at the ILV2 locus of chromosome XIII in Saccharomyces cerevisiae.

Rank GH; Arndt GM; Xiao W

Department of Biology, University of Saskatchewan, Saskatoon, Canada.

Curr Genet Feb 1989, 15 (2) p107-12, ISSN 0172-8083 Journal Code: CUG

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/20 (Item 20 from file: 155)

06876684 89178684

FLP recombinase of the 2 microns circle plasmid of Saccharomyces cerevisiae bends its DNA target. Isolation of FLP mutants defective in DNA bending.

Schwartz CJ; Sadowski PD

Department of Medical Genetics, University of Toronto, Ontario, Canada.

J Mol Biol Feb 20 1989, 205 (4) p647-58, ISSN 0022-2836

Journal Code: J6V Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/21 (Item 21 from file: 155)

06825220 89127220

Holliday intermediates and reaction by-products in FLP protein-promoted site-specific recombination.

Meyer-Leon L; Huang LC; Umlauf SW; Cox MM; Inman RB

Department of Biochemistry, College of Agriculture and Life Sciences, University of Wisconsin-Madison 53706-1569.

Mol Cell Biol Sep 1988, 8 (9) p3784-96, ISSN 0270-7306

Journal Code: NGY

Contract/Grant No.: GM37835; GM14711

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/22 (Item 22 from file: 155)

06823587 89125587

The mechanism of loading of the FLP recombinase onto its DNA target sequence.

Beatty LG: Sadowski PD

Department of Medical Genetics, University of Toronto, Ontario, Canada.

J Mol Biol Nov 20 1988, 204 (2) p283-94, ISSN 0022-2836

Journal Code: J6V

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/23 (Item 23 from file: 155)

06794920 89096920

Step-arrest mutants of FLP recombinase: implications for the catalytic mechanism of DNA recombination.

Parsons RL; Prasad PV; Harshey RM; Jayaram M

Department of Molecular Biology, Research Institute of Scripps Clinic, La Jolla, California 92037.

Aug 1988, 8 (8) p3303-10, ISSN 0270-7306 Mol Cell Riol

Journal Code: NGY

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/24 (Item 24 from file: 155)

06761437 89063437

High frequency FLP-independent homologous DNA recombination of 2 mu plasmid in the yeast Saccharomyces cerevisiae.

Bruschi CV; Howe GA

Department of Microbiology and Immunology, School of Medicine, East Carolina University, Greenville, NC 27858-4354.

Curr Genet Sep 1988, 14 (3) p191-9, ISSN 0172-8083 Journal Code: CUG

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/25 (Item 25 from file: 155)

06740094 89042094

Holliday junctions in FLP recombination: resolution by step-arrest mutants of FLP protein.

Jayaram M; Crain KL; Parsons RL; Harshey RM

Department of Molecular Biology, Research Institute of Scripps Clinic, La Jolla, CA 92037.

Proc Natl Acad Sci U S A Nov 1988, 85 (21) p7902-6, ISSN 0027-8424 Journal Code: PV3

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/26 (Item 26 from file: 155)

06703077 89005077

The functional significance of DNA sequence structure in a site-specific genetic recombination reaction.

Umlauf SW; Cox MM

Department of Biochemistry, College of Agricultural and Life Sciences, University of Wisconsin-Madison 53706.

Jun 1988, 7 (6) p1845-52, ISSN 0261-4189 Journal Code: EMB Contract/Grant No.: GM37835; AI00599; GM07215

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/27 (Item 27 from file: 155)

06687975 88332975

DNA recognition by the FLP recombinase of the yeast 2 mu plasmid. A mutational analysis of the FLP binding site.

Senecoff JF; Rossmeissl PJ; Cox MM

Department of Biochemistry, College of Agricultural and Life Sciences, University of Wisconsin-Madison 53706.

May 20 1988, 201 (2) p405-21, ISSN 0022-2836 J Mol Biol Journal Code: J6V

Contract/Grant No.: GM37835; AI00599

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/28 (Item 28 from file: 155)

06643050 88288050

Nucleotide sequencing and expression of the fadL gene involved in long-chain fatty acid transport in Escherichia coli.

Said B; Ghosn CR; Vu L; Nunn WD

Department of Molecular Biology and Biochemistry, University of California, Irvine 92717.

Mol Microbiol May 1988, 2 (3) p363-70, ISSN 0950-382X

Journal Code: MOM

Contract/Grant No.: GM 22466-11

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/29 (Item 29 from file: 155)

06618001 88263001

FLP recombinase is an enzyme.

Gates CA: Cox MM

Department of Biochemistry, College of Agricultural and Life Sciences, University of Wisconsin-Madison 53706.

Proc Natl Acad Sci U S A Jul 1988, 85 (13) p4628-32, ISSN 0027-8424 Journal Code: PV3

Contract/Grant No.: GM37835; AI00599

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/30 (Item 30 from file: 155)

06567126 88212126

Mutations that improve the binding of yeast FLP recombinase to its ${\mathbb R}^2$ substrate.

Lebreton B; Prasad PV; Jayaram M; Youderian P

Department of Biological Sciences, University of Southern California, Los Angeles 90089-1481.

Genetics Mar 1988, 118 (3) p393-400, ISSN 0016-6731 Journal Code: FNH

Contract/Grant No.: GM34982; GM35654

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/31 (Item 31 from file: 155)

06521666 88166666

Antagonistic controls regulate copy number of the yeast 2 mu plasmid.

Murray JA; Scarpa M; Rossi N; Cesareni G

EMBL, Heidelberg, FRG.

EMBO J Dec 20 1987, 6 (13) p4205-12, ISSN 0261-4189 Journal Code: EMB

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/32 (Item 32 from file: 155)

06506025 88151025

Autoregulation of 2 micron circle gene expression provides a model for

maintenance of stable plasmid copy levels.

Som T; Armstrong KA; Volkert FC; Broach JR

Department of Molecular Biology, Princeton University, New Jersey 08544.

Cell Jan 15 1988, 52 (1) p27-37, ISSN 0092-8674 Journal Code: CQ4

Contract/Grant No.: GM34596

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/33 (Item 33 from file: 155)

06342913 87316913

Purification of the FLP site-specific recombinase by affinity chromatography and re-examination of basic properties of the system.

Meyer-Leon L; Gates CA; Attwood JM; Wood EA; Cox MM

Nucleic Acids Res Aug 25 1987, 15 (16) p6469-88, ISSN 0305-1048

Journal Code: O&L

Contract/Grant No.: GM32335; GM37835; AI00599; +

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/34 (Item 34 from file: 155)

06280212 87254212

Isolation of intermediates in the binding of the FLP recombinase of the yeast plasmid 2-micron circle to its target sequence.

Andrews BJ; Beatty LG; Sadowski PD

J Mol Biol Jan 20 1987, 193 (2) p345-58, ISSN 0022-2836

Journal Code: J6V

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/35 (Item 35 from file: 155)

06274060 87248060

Rapid localization and characterization of random mutations within the 2 micron circle site-specific recombinase: a general strategy for analysis of protein function [published erratum appears in Gene 1987:57(1):149]

Govind NS: Jayaram M

Gene 1987, 51 (1) p31-41, ISSN 0378-1119 Journal Code: FOP

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/36 (Item 36 from file: 155)

06210407 87184407

Site-specific recombination of the yeast plasmid two-micron circle: intermediates in the binding process.

Andrews BJ; Beatty LG; Sadowski PD

Basic Life Sci 1986, 40 p407-24, ISSN 0090-5542 Journal Code: 9K0

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/37 (Item 37 from file: 155)

06210406 87184406

Site-specific recombination promoted in vitro by the FLP protein of the yeast two-micron plasmid.

Senecoff JF; Bruckner RC; Meyer-Leon L; Gates CA; Wood E; Umlauf SW; Attwood JM; Cox MM

Basic Life Sci 1986, 40 p397-405, ISSN 0090-5542 Journal Code: 9K0

Contract/Grant No.: GM32335; 5-T32 GM07215; AI00599

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/38 (Item 38 from file: 155)

06210404 87184404

Survival strategies of the yeast plasmid two-micron circle.

Volkert FC; Wu LC; Fisher PA; Broach JR

Basic Life Sci 1986, 40 p375-96, ISSN 0090-5542 Journal Code: 9K0

Contract/Grant No.: GM34596; GM33132

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/39 (Item 39 from file: 155)

06201639 87175639

Mutations in the 2-microns circle site-specific recombinase that abolish recombination without affecting substrate recognition [published erratum appears in Proc Natl Acad Sci U S A 1988 Mar;85(5):1497]

Prasad PV; Young LJ; Jayaram M

Proc Natl Acad Sci U S A Apr 1987, 84 (8) p2189-93, ISSN 0027-8424

Journal Code: PV3

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/40 (Item 40 from file: 155)

06167165 87141165

Association of reciprocal exchange with gene conversion between the repeated segments of 2-micron circle.

Jayaram M

J Mol Biol Oct 5 1986, 191 (3) p341-54, ISSN 0022-2836

Journal Code: J6V Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/41 (Item 41 from file: 155)

06115790 87089790

Substrate recognition by the 2 micron circle site-specific recombinase: effect of mutations within the symmetry elements of the minimal substrate.

Prasad PV; Horensky D; Young LJ; Jayaram M

Mol Cell Biol Dec 1986, 6 (12) p4329-34, ISSN 0270-7306

Journal Code: NGY

Contract/Grant No.: GM 35654-01

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/42 (Item 42 from file: 155)

06115725 87089725

Mating type-like conversion promoted by the 2 micrograms circle site-specific recombinase: implications for the double-strand-gap repair model.

Jayaram M

Mol Cell Biol Nov 1986, 6 (11) p3831-7, ISSN 0270-7306 Journal Code: NGY Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/43 (Item 43 from file: 155)

06115667 87089667

Identification of the crossover site during FLP-mediated recombination in the Saccharomyces cerevisiae plasmid 2 microns circle.

McLeod M; Craft S; Broach JR

Mol Cell Biol Oct 1986, 6 (10) p3357-67, ISSN 0270-7306

Journal Code: NGY Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/44 (Item 44 from file: 155)

06090546 87064546

Interaction of the FLP recombinase of the Saccharomyces cerevisiae 2 micron plasmid with mutated target sequences.

Andrews BJ; McLeod M; Broach J; Sadowski PD

Mol Cell Biol Jul 1986, 6 (7) p2482-9, ISSN 0270-7306

Journal Code: NGY

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/45 (Item 45 from file: 155)

06009798 86310798

The FLP recombinase of the Saccharomyces cerevisiae 2 microns plasmid attaches covalently to DNA via a phosphotyrosyl linkage.

Gronostajski RM; Sadowski PD

Mol Cell Biol Nov 1985, 5 (11) p3274-9, ISSN 0270-7306

Journal Code: NGY Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/46 (Item 46 from file: 155)

06003314 86304314

Specific contacts between the FLP protein of the yeast 2-micron plasmid and its recombination site.

Bruckner RC; Cox MM

J Biol Chem Sep 5 1986, 261 (25) p11798-807, ISSN 0021-9258

Journal Code: HIV

Contract/Grant No.: GM32335; AI00599

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/47 (Item 47 from file: 155)

05983659 86284659

Chromatin organization of the Saccharomyces cerevisiae 2 microns plasmid depends on plasmid-encoded products.

Veit BE; Fangman WL

Mol Cell Biol Sep 1985, 5 (9) p2190-6, ISSN 0270-7306

Journal Code: NGY

Contract/Grant No.: GM18926

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/48 (Item 48 from file: 155)

05980709 86281709

FLP site-specific recombinase of yeast 2-micron plasmid. Topological features of the reaction.

Beatty LG; Babineau-Clary D; Hogrefe C; Sadowski PD

J Mol Biol Apr 20 1986, 188 (4) p529-44, ISSN 0022-2836

Journal Code: J6V

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/49 (Item 49 from file: 155)

05971102 86272102

Site-specific recombination promotes plasmid amplification in yeast.

Volkert FC; Broach JR

Cell Aug 15 1986, 46 (4) p541-50, ISSN 0092-8674 Journal Code: CQ4

Contract/Grant No.: GM-34596

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/50 (Item 50 from file: 155)

05958059 86259059

The minimal duplex DNA sequence required for site-specific recombination promoted by the FLP protein of yeast in vitro.

Proteau G; Sidenberg D; Sadowski P

Nucleic Acids Res Jun 25 1986, 14 (12) p4787-832, ISSN 0305-1048

Journal Code: O8L

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/51 (Item 51 from file: 155)

05931585 86232585

Sequence organization of the circular plasmid pKD1 from the yeast Kluyveromyces drosophilarum.

Chen XJ; Saliola M; Falcone C; Bianchi MM; Fukuhara H

Nucleic Acids Res Jun 11 1986, 14 (11) p4471-81, ISSN 0305-1048

Journal Code: O&L

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/52 (Item 52 from file: 155)

05923006 86224006

Directionality in FLP protein-promoted site-specific recombination is mediated by DNA-DNA pairing.

Senecoff JF; Cox MM

J Biol Chem Jun 5 1986, 261 (16) p7380-6, ISS 4 0021-9258

Journal Code: HIV

Contract/Grant No.: GM32335; AI00599

Languages: ENGLISH

Document type: JOURNAL ARTICLE

2/3/53 (Item 53 from file: 155)

05919123 86220123

The integrase family of site-specific recombinase; regional similarities

and global diversity. Argos P; Landy A; Abremski K; Egan JB; Haggard Ljungquist E; Hoess RH; Kahn ML; Kalionis B; Narayana SV; Pierson LS 3d; et al EMBO J Feb 1986, 5 (2) p433-40, ISSN 0261-418) Journal Code: EMB Contract/Grant No.: AI 13544 Languages: ENGLISH Document type: JOURNAL ARTICLE 2/3/54 (Item 54 from file: 155) 05810590 86111590 Site-specific recombinases: changing partners and doing the twist. Sadowski P J Bacteriol Feb 1986, 165 (2) p341-7, ISSN 0321-9193 Journal Code: ннз Languages: ENGLISH Document type: JOURNAL ARTICLE; REVIEW 2/3/55 (Item 55 from file: 155) 05741647 86042647 The FLP recombinase of the yeast 2-micron plasmid: characterization of its recombination site. Senecoff JF; Bruckner RC; Cox MM Proc Natl Acad Sci U S A Nov 1985, 82 (21) p72/0-4, ISSN 0027-8424 Journal Code: PV3 Contract/Grant No.: GM32335 Languages: ENGLISH Document type: JOURNAL ARTICLE 2/3/56 (Item 56 from file: 155) 05707309 86008309 The FLP protein of the 2-micron plasmid of yeast. Interintramolecular reactions. Gronostajski RM; Sadowski PD J Biol Chem Oct 5 1985, 260 (22) p12328-35, IBSN 0021-9258 Journal Code: HIV Languages: ENGLISH Document type: JOURNAL ARTICLE 2/3/57 (Item 57 from file: 155) 05707308 86008308 Determination of DNA sequences essential for FL 3-mediated recombination by a novel method. Gronostajski RM; Sadowski PD J Biol Chem Oct 5 1985, 260 (22) p12320-7, ISBN 0021-9258 Journal Code: HIV Languages: ENGLISH Document type: JOURNAL ARTICLE 2/3/58 (Item 58 from file: 155) 05707307 86008307 The FLP protein of the 2-micron plasmid of yeast. Purification of the protein from Escherichia coli cells expressing the cloned FLP gene. Babineau D; Vetter D; Andrews BJ; Gronostajski RM; Proteau GA; Beatty LG;

Sadowski PD

J Biol Chem Oct 5 1985, 260 (22) p12313-9, ISSN 0021-9258 Journal Code: HIV Languages: ENGLISH Document type: JOURNAL ARTICLE 2/3/59 (Item 59 from file: 155) 05560933 85176933 The FLP recombinase of the 2 micron circle DNA of yeast: interaction with its target sequences. Andrews BJ; Proteau GA; Beatty LG; Sadowski PD Apr 1985, 40 (4) p795-803, ISSN 0092-8674 Journal Code: CQ4 Languages: ENGLISH Document type: JOURNAL ARTICLE (Item 1 from file: 5) 2/3/60 BIOSIS Number: 42131509 8906509 _ AN ORDERED DISASSEMBLY OF COMPLEXES OF FLP RECOMBINASE AND FRT SITES FOLLOWING RECOMBINATION WAITE L L; COX M M DEP. BIOCHEM., UNIV. WISCONSTH, MADISON, WIS. 53706. KEYSTONE SYMPOSIUM ON MOLECULAR MECHANISMS IN DNG REPLICATION AND RECOMBINATION, TAOS, NEW MEXICO, USA, JANDARY 25-FI BRUARY 1. 1992. J CELL BIOCHEM SUPPL 0 (16 PART B). 1992. 67. CODEN: J(BSD Language: ENGLISH Document Type: CONFERENCE PAPER 2/3/61 (Item 2 from file: 5) 8906501 BIOSIS Number: 42131501 LIGATION ACTIVITY OF THE FLP RECOMBINASE PAN G; SADOWSKI P D DEP. MOLECULAR MED. GENETICS, UNIV. TORONTO, TORONTO, ONTARIO M5S 1A8, CAN. KEYSTONE SYMPOSIUM ON MOLECULAR MECHANISMS IN DN/ REPLICATION AND RECOMBINATION, TAOS, NEW MEXICO, USA, JANUARY 25-FIBRUARY 1, 1992. J CELL BIOCHEM SUPPL 0 (16 PART B). 1992. 65. CODEN: J(BSD Language: ENGLISH Document Type: CONFERENCE PAPER 2/3/62 (Item 3 from file: 5) 8906498 BIOSIS Number: 42131498 HALF-SITE RECOMBINATIONS MEDIATED BY FLP RECOMBINASE FROM SACCHAROMYCES-CEREVISIAE SERRE M-C; LEI-ZHENG; JAYARAM M DEP. MICROBIOL., UNIV. TEXAS AUSTIN, AUSTIN, TEX. 78746. KEYSTONE SYMPOSIUM ON MOLECULAR MECHANISMS IN DNF REPLICATION AND RECOMBINATION, TAOS, NEW MEXICO, USA, JANUARY 25-FEBRUARY 1, 1992. J CELL BIOCHEM SUPPL 0 (16 PART B). 1992. 64. CODEN: J(BSD Language: ENGLISH Document Type: CONFERENCE PAPER 2/3/63

/3/63 (Item 4 from file: 5) 06492 BIOSIS Number: 42131492 FUNCTIONAL ANALYSES OF MUTANTS OF FLP AND R RECOMBINASE FROM YEAST CHEN J-W; LEE J; EVANS B; SERRE M-C; ARAKI H; OSPIMA Y; JAYARAM M DEP. MICROBIOL., UNIV. TEXAS AUSTIN, AUSTIN, TEX. 78712.
KEYSTONE SYMPOSIUM ON MOLECULAR MECHANISMS IN DNA REPLICATION AND
RECOMBINATION, TAOS, NEW MEXICO, USA, JANUARY 25-FEBRUARY 1, 1992. J CELL
BIOCHEM SUPPL 0 (16 PART B). 1992. 62. CODEN: JCBSD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/64 (Item 5 from file: 5) 8197568 BIOSIS Number: 91118568

TYROSINE-60 VARIANTS OF FLP RECOMBINASE GENERATE CONFORMATIONALLY ALTERED PROTEIN DNA COMPLEXES DIFFERENTIAL ACTIVITY IN FULL-SITE AND HALF RECOMBINATIONS

CHEN J-W; EVANS B R; ZHENG L; JAYARAM M
DEP. MICRBOIOL., UNIV. TEXAS AUSTIN, AUSTIN, TEX. 78712, USA.
J MOL BIOL 218 (1). 1991. 107-118. CODEN: JMORA
Full Journal Title: Journal of Molecular Biology
Language: ENGLISH

2/3/65 (Item 6 from file: 5) 7103760 BIOSIS Number: 88026505

FLP-FRT MEDIATED INTRACHROMOSOMAL RECOMBINATION ON A TANDEMLY DUPLICATED YE-P INTEGRANT AT THE ILV2 LOCUS OF CHROMOSOME XIII IN SACCHAROMYCES-CEREVISIAE

RANK G H; ARNDT G M; XIAO W

DEP. BIOL., UNIV. SASKATCHEWAN, SASKATOON, SASKATCHEWAN, CANADA S7N 0W0. CURR GENET 15 (2). 1989. 107-112. CODEN: CUGED Full Journal Title: Current Genetics Language: ENGLISH

2/3/66 (Item 7 from file: 5) 7043154 BIOSIS Number: 87103675

FLP RECOMBINASE OF THE 2 MUM CIRCLE PLASMID OF SACCHAROMYCES-CEREVISIAE BENDS ITS DNA TARGET ISOLATION OF FLP MUTANTS DEFECTIVE IN DNA BENDING SCHWARTZ C J E; SADOWSKI P D

DEP. MED. GENETICS, UNIV. TORONTO, TORONTO, ONTARIO M5S 1A8, CAN. J MOL BIOL 205 (4). 1989. 647-658. CODEN: JMOBA Full Journal Title: Journal of Molecular Biology Language: ENGLISH

2/3/67 (Item 8 from file: 5) 6944460 BIOSIS Number: 87004981

HIGH FREQUENCY FLP-INDEPENDENT HOMOLOGOUS DNA RECOMBINATION OF 2 MICRON PLASMID IN THE YEAST SACCHAROMYCES-CEREVISIAE

BRUSCHI C V: HOWE G A

DEP. MICROBIOL. IMMUNOL., SCH. MED., EAST CAROLINA UNIV., GREENVILLE, N.C. 27858-4354, U.S.A.

CURR GENET 14 (3). 1988. 191-200. CODEN: CUGED

Full Journal Title: Current Genetics Language: ENGLISH

2/3/68 (Item 9 from file: 5) 892306 BIOSIS Number: 37086685

THE FLP RECOMBINASE STEP-ARREST MUTANTS AND INTERMEDIATES IN RECOMBINATION

JAYARAM M; PARSONS R; EVANS B

RES. INST. SCRIPPS CLIN., LA JOLLA, CALIF. 92037.

SYMPOSIUM ON MOLECULAR MECHANISMS IN DNA R PLICATION AND RECOMBINATION HELD AT THE 18TH ANNUAL UCLA (UNIVERSITY OF ALIFORNIA-LOS ANGELES) SYMPOSIA ON MOLECULAR AND CELLULAR BIOLOGY, TEAMBOAT SPRINGS, COLORADO, USA, MARCH 27-APRIL 3, 1989. J CELL BIOCHEM UPPL Ø (13 PART D). 1989. 106. CODEN: JCBSD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/69 (Item 10 from file: 5)

6636107 BIOSIS Number: 86102658

AUTOREGULATION OF 2-MUM CIRCLE GENE EXPRES ION PROVIDES A MODEL FOR MAINTENANCE OF STABLE PLASMID COPY LEVELS

SOM T; ARMSTRONG K A; VOLKERT F C; BROACH J R

DEP. MOLECULAR BIOL., PRINCETON UNIV., PRINCETON, NEW JERSEY 08544.

CELL 52 (1). 1988. 27-38. CODEN: CELLB

Full Journal Title: Cell

Language: ENGLISH

2/3/70 (Item 11 from file: 5)

6624830 BIOSIS Number: 86091381

THE INT FAMILY OF SITE-SPECIFIC RECOMBINASES SOME THOUGHTS ON A GENERAL REACTION MECHANISM

JAYARAM M

DEP. MOL. BIOL., RES. INST. SCRIPPS CLINIC, 10666 NORTH TORREY PINES ROAD, LA JOLLA, CALIF. 92037, USA.

J GENET 67 (1). 1988. 29-36. CODEN: JOGIA

Full Journal Title: Journal of Genetics

Language: ENGLISH

2/3/71 (Item 12 from file: 5)

6571174 BIOSIS Number: 86037725

FLP RECOMBINASE INDUCTION OF THE BREAKAGE-FUSION-BRIDGE CYCLE AND GENE CONVERSION IN SACCHAROMYCES-CEREVISIAE

RANK G H; XIAO W; KOLENOVSKY A; ARNDT G

DEP. BIOL., UNIV. SASK., SASKATOON, SASK., CAN. S7N OWO.

CURR GENET 13 (4). 1988. 273-282. CODEN: CUGED

Full Journal Title: Current Genetics

Language: ENGLISH

2/3/72 (Item 13 from file: 5)

6150196 BIOSIS Number: 35015717

PURIFICATION OF FLP RECOMBINASE USING SEQUENCE-SPECIFIC DNA AFFINITY CHROMATOGRAPHY

GATES C A; MEYER-LEON L; ATTWOOD J M; WOOD E A; COX M M

DEP. BIOCHEM., UNIV. WIS.-MADISON, MADISON, WIS. 53706, USA.

BURGESS, R. (ED.). UCLA (UNIVERSITY OF CALIFORNIA-LOS ANGELES) SYMPOSIA ON MOLECULAR AND CELLULAR BIOLOGY NEW SERIES, VOL. 68. PROTEIN PURIFICATION: MICRO TO MACRO; CETUS-UCLA SYMFOSIUM, FRISCO, COLORADO, USA, MARCH 29-APRIL 4, 1987. XVIII+510P. ALAN R. LISS, INC.: NEW YORK, NEW YORK, USA. ILLUS. ISBN 0-8451-2667-9. 0 (0). 1987. 197-206. CODEN: USMBD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/73 (Item 14 from file: 5)

5802738 BIOSIS Number: 83065045

SUBSTRATE RECOGNITION BY THE 2-MICROMETER CIRCLE SITE-SPECIFIC RECOMBINASE EFFECT OF MUTATIONS WITHIN THE SYMMETRY ELEMENTS OF THE MINIMAL SUBSTRATE

PRASAD P V; HORENSKY D; YOUNG L-J; JAYARAM M
DEP. MOL. BIOL., RES. INST. SCRIPPS CLIN., LA JOLLA, CALIF. 92037, USA.
MOL CELL BIOL 6 (12). 1986. 4329-4334. CODEN: MCEBD
Full Journal Title: Molecular and Cellular Biology

Language: ENGLISH

2/3/74 (Item 15 from file: 5)

5761770 BIOSIS Number: 83024077

MATING TYPE-LIKE CONVERSION PROMOTED BY THE 2 MICROMETER CIRCLE SITE-SPECIFIC RECOMBINASE IMPLICATIONS FOR THE 'DOUBLE-STRAND-GAP REPAIR MODEL

JAYARAM M

DEP. MOLECULAR BIOLOGY, RESEARCH INST. SCRIPPS CLINIC, LA JOLLA, CALIFORNIA 92037.

MOL CELL BIOL 6 (11). 1986. 3831-3837. CODEN: MCEBD Full Journal Title: Molecular and Cellular Biology Language: ENGLISH

2/3/75 (Item 16 from file: 5) 5751545 BIOSIS Number: 83013852

ASSOCIATION OF RECIPROCAL EXCHANGE WITH GENE CONVERSION BETWEEN THE REPEATED SEGMENTS OF 2-MICROMETER CIRCLE
JAYARAM M

DEPARTMENT OF MOLECULAR BIOLOGY, RESEARCH INSTITUTE OF SCRIPPS CLINIC, 10666 NORTH TORREY PINES ROAD, LA JOLLA, CALIF. 92037, USA. J MOL BIOL 191 (3). 1986. 341-354. CODEN: JMOBA Full Journal Title: Journal of Molecular Biology

Language: ENGLISH

2/3/76 (Item 17 from file: 5) 5696494 BIOSIS Number: 33091515

MECHANISMS OF ACTION OF THE FLP RECOMBINASE OF THE 2-MICRON PLASMID OF YEAST

SADOWSKI P D; BEATTY L G; CLARY D; OLLERHEAD S

DEP. MED. GENETICS, MED. SCIENCES BUILD., UNIV. TORONTO, TORONTO, CANADA M5S 1A8.

MCMACKEN, R. AND T. J. KELLY (ED.). UCLA (UNIVERSITY OF CALIFORNIA-LOS ANGELES) SYMPOSIA ON MOLECULAR AND CELLULAR BIOLOGY NEW SERIES, VOL. 47. DNA REPLICATION AND RECOMBINATION; PARK CITY, UTAH, USA, MARCH 16-23, 1986. XXVI+782P. ALAN R. LISS, INC.: NEW YORK, NEW YORK, USA. ILLUS. ISBN 0-8451-2646-6. 0 (0). 1987. 691-702. CODEN: USMBD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/77 (Item 18 from file: 5) 5504855 BIOSIS Number: 32027162

INTERACTION OF THE FLP RECOMBINASE OF THE 2-MICRON PLASMID WITH ITS TARGET SEQUENCE

SADOWSKI P D; ANDREWS B J; BEATTY L G; SIDENBERG D; PROTEAU G DEP. MED. GENETICS, UNIV. TORONTO, TORONTO M5S 1A8, CAN.

KLAR, A. AND J. N. STRATHERN (ED.). CURRENT COMMUNICATIONS IN MOLECULAR BIOLOGY: MECHANISMS OF YEAST RECOMBINATION; MEETING, COLD SPRING HARBOR, N.Y., USA. IX+193P. COLD SPRING HARBOR LABORATORY: COLD SPRING HARBOR. N.Y., USA. ILLUS. PAPER. ISBN 0-87969-195-6. 0 (0). 1986. 7-10. CODEN: 24607

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/78 (Item 19 from file: 5)

5426144 BIOSIS Number: 82070947

INTERACTION OF THE FLP RECOMBINASE OF THE SACCHAROMYCES-CEREVISIAE 2 MICROMETER PLASMID WITH MUTATED TARGET SEQUENCES

ANDREWS B J; MCLEOD M; BROACH J; SADOWSKI P D

DEP. OF MED. GENETICS, UNIV. OF TORONTO, TORONTO, ONTARIO M5S 1A8,

MOL CELL BIOL 6 (7). 1986. 2482-2489. CODEN: MCEBD Full Journal Title: Molecular and Cellular Biology Language: ENGLISH

2/3/79 (Item 20 from file: 5) 5389362 BIOSIS Number: 82034165

FLP SITE-SPECIFIC RECOMBINASE OF YEAST 2-MICROMETER PLASMID TOPOLOGICAL FEATURES OF THE REACTION

BEATTY L G; BABINEAU-CLARY D; HOGREFE C; SADOWSKI P D DEP. OF MED. GENETICS, UNIV. OF TORONTO, TORONTO M5S 1A8, CANADA. J MOL BIOL 188 (4). 1986. 529-544. CODEN: JMORA

Full Journal Title: Journal of Molecular Biology

Language: ENGLISH

2/3/80 (Item 21 from file: 5)

BIOSIS Number: 81033120

THE FLP RECOMBINASE OF THE SACCHAROMYCES-CEREVISIAE 2 MIDROMETER PLASMID ATTACHES COVALENTLY TO DNA VIA A PHOSPHOTYROSYL LINKAGE

GRONOSTAJSKI R M; SADOWSKI P D

DEP. MED. GENET., UNIV. TORONTO, TORONTO, ONT. M5S1A8, CHN. MOL CELL BIOL 5 (11). 1985. 3274-3279. CODEN: MCEBD Full Journal Title: Molecular and Cellular Biology

Language: ENGLISH

2/3/81 (Item 22 from file: 5) 5256098 BIOSIS Number: 81023405

THE FLP PROTEIN OF THE 2-MICRON PLASMID OF YEAST SACCHAR MYCES-CEREVISIAE PURIFICATION OF THE PROTEIN FROM ESCHERICHIA-COLI CELLS EX! RESSING THE CLONED FLP GENE

BABINEAU D; VETTER D; ANDREWS B J; GRONOSTAJSKI R M; PROJEAU G A; BEATTY L G; SADOWSKI P D

DEP. MED. GENETICS, UNIV. TORONTO, TORONTO, M59 1A8, CANDA. J BIOL CHEM 260 (22). 1985. 12313-12319. CODEN: JBCHA Full Journal Title: Journal of Biological Chemistry

Language: ENGLISH

2/3/82 (Item 23 from file: 5) 5168213 BIOSIS Number: 31057528

THE FLP RECOMBINASE OF THE 2-MICRON PLASMID OF YEAST

SADOWSKI P D; ANDREWS B J; BABINEAU-CLARY D; BEATTY L; GRONOSTAJSKI R M; PROTEAU G; SIDENBERG D

DEF. MED. GENET., UNIV. TORONTO, TORONTO M5S 1A8, CANADA.

SYMPOSIUM ON MECHANISMS OF DNA REPLICATION AND RECOMBINATION HELD AT THE 15TH ANNUAL MEETING OF THE UCLA (UNIVERSITY OF CALIFORNIA-LOS ANGELES) SYMPOSIA ON MOLECULAR AND CELLULAR BIOLOGY, MAR. 16-23, 1986. J CELL BIOCHEM SUPPL 0 (10 PART E). 1986. 137. CODEN: JCBSD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/83 (Item 24 from file: 5) 4696890 BIOSIS Number: 29054205

INTERACTION OF THE FLP RECOMBINASE WITH SUBSTRATE 2-MICRON CIRCLE DNA ANDREWS B J; BEATTY L; SADOWSKI P D UNIV. TORONTO.

SYMPOSIUM ON YEAST CELL BIOLOGY HELD AT THE 14TH ANNUAL MEETING OF THE UCLA (UNIVERSITY OF CALIFORNIA - LOS ANGELES) SYMPOSIA ON MOLECULAR AND CELLULAR BIOLOGY, APR. 9-15, 1985. J CELL BIOCHEM SUPPL Ø (9 PART C). 1985. 117. CODEN: JCBSD

Language: ENGLISH

Document Type: CONFERENCE PAPER

2/3/84 (Item 1 from file: 399)

116167825 CA: 116(17)167825y PATENT

Methods for in vitro recombination of multigene families for generation of new phenotypes

INVENTOR(AUTHOR): Short, Jay M.; Sorge, Joseph A.

LOCATION: USA

ASSIGNEE: Stratagene

PATENT: PCT International; WO 9116427 A1 DATE: 911031 APPLICATION: WO 91US2910 (910424) *US 513957 (900424)

FAGES: 204 pp. CODEN: PIXXD2 LANGUAGE: English CLASS: C12N-015/00A; C12P-019734B; C12P-021/06B; C07H-021/00B DESIGNATED COUNTRIES: AU; CA; FI; JP; KR; NO DESIGNATED REGIONAL: AT; BE; CH; DE; DK; ES; FR; GB; GR; IT; LU; NL; SE

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2/3/85 (Item 2 from file: 399)

106208826 CA: 106(25)208826p JOURNAL

Rapid localization and characterization of random mutations within the 2.mu. circle site-specific recombinase: a general strategy for analysis of protein function

AUTHOR(S): Govind, Nadathur S.; Jayaram, Makkuni

LOCATION: Res. Inst. Scripps Clin., La Jolla, CA, 92037, USA

JOURNAL: Gene DATE: 1987 VOLUME: 51 NUMBER: 1 PAGES: 31-41 CODEN: GENED6 ISSN: 0378-1119 LANGUAGE: English

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2/3/86 (Item 3 from file: 399)

104001445 CA: 104(1)1445b JOURNAL

The FLP recombinase of the yeast 2-.mu.m plasmid: characterization of its recombination site AUTHOR(S): Senecoff, Julie F.; Bruckner, Robert C.; Cox, Michael M. LOCATION: Coll. Agric. Life Sci., Univ. Wisconsin, Madison, WI. 53706. JOURNAL: Proc. Natl. Acad. Sci. U. S. A. DATE: 1985 VOLUME: 82 NUMBER: 21 PAGES: 7270-4 CODEN: PNASA6 ISSN: 0027-8424 LANGUAGE: English Copyright 1992 by the American Chemical Society 2/3/87 (Item 4 from file: 399) 102216080 CA: 102(25)216080y JOURNAL The FLF recombinase of the 2.mu. circle DNA of yeast: interaction with its target sequences AUTHOR(S): Andrews, Brenda J.; Proteau, Gerald A.; Beatty, Linda G.; Sadowski, Paul D. LOCATION: Dep. Med. Genet., Univ. Toronto, Toronto, ON, Can., M5S 1A8 JOURNAL: Cell (Cambridge, Mass.) DATE: 1985 VOLUME: 40 NUMBER: 4 PAGES: 795-803 CODEN: CELLES ISSN: 0092-8674 LANGUAGE: English Copyright 1992 by the American Chemical Society 2/3/88 (Item 1 from #1e: 434) 11506141 Genuine Article#: HN234 No. References: 35 Title: SITE-SPECIFIC RECOMBINATION OF 2-MU-M PLASMID OF YEAST SACCHAROMYRES-CEREVISIAE Author(s): FUSHNOVA EA Corporate Source: ST PETERBURG PEDIAT MED INST/ST PETERBURG//USSR/ Joury 1: GENETIKA, 1992, V28, N2 (FEB), P25-34 Language: RUSSIAN Document Type: ARTICLE (Abstract Available) 2/3/89 (Item 2 from file: 434) 11487805 Genuine Article#: HM053 No. References: 33 Title: SITE-SPECIFIC INTEGRATION OF THE HAEMOPHILUS-INFLUENZAE BACTERIOPHAGE HP1 - IDENTIFICATION OF THE POINTS OF RECOMBINATIONAL STRAND EXCHANGE AND THE LIMITS OF THE HOST ATTACHMENT SITE Author(s): HAUSER MA; SCOCCA JJ Corporate Source: JOHNS HOPKINS UNIV, SCH HYG & PUBL HLTH, DEPT BIOCHEM/BALTIMORE//MD/21205; JOHNS HOPKINS UNIV, SCH HYG & PUBL HLTH, DEPT BIOCHEM/BALTIMORE//MD/21205 Journal: JOURNAL OF BIOLOGICAL CHEMISTRY, 1992, V267, N10 (APR 5), P 6859-6864 Language: ENGLISH Document Type: ARTICLE (Abstract Available) 2/3/90 (Item 3 from file: 434) 11338662 Genuine Article#: HB304 / No. References: 21 Title: EXCHANGE OF GENE ACTIVITY IN TRANSGENIC PLANTS CATALYZED BY THE CRE-LOX SITE-SPECIFIC RECOMBINATION SYSTEM Author(s): BAYLEY CC; MORGAN JX; DALE EC; OW DW Corporate Source: USDA ARS, ETR PLANT GENE EXPRESS, 800 BUCHANAN ST/ALBANY//CA/94710; USDA ARS, CTR PLANT GENE EXPRESS, 800 BUCHANAN

ST/ALBANY//CA/94718; UNIV CALIF BERKELEY, DEPT PLANT

PATHOL/BERKELEY/CA/94720

Journal: PLANT MOLECULAR BIOLOGY, 1992, V18, N2 (JAN), P353-361 Language: ENGLISH Document Type: ARTICLE (Abstract Available) 2/3/91 (Item 4 from file: 434) 11317754 Genuine Article#: GZ516 No. References: 33 Title: A FROG VIRUS-3 GENE CODES FOR A PROTEIN CONTAINING THE MOTIF CHARACTERISTIC OF THE INT FAMILY OF INTEGRASES Author(s): ROHOZINSKI J; GOORHA R Corporate Source: ST JUDE CHILDRENS HOSP, DEPT VIROL & MOLEC BIOL, 332 N LAUDERDALE, POB 318/MEMPHIS//TN/38101; ST JUDE CHILDRENS HOSP, DEPT VIROL & MOLEC BIOL, 332 N LAUDERDALE, POB 318/MEMPHIS//TN/38101 Journal: VIROLOGY, 1992, V186, N2 (FEB), P693-700 Language: ENGLISH Document Type: ARTICLE 2/3/92 (Item 5 from file: 434) 10583597 Genuine Article#: EP811 No. References: 61 Title: A NOVEL RECOMBINATOR IN YEAST BASED ON GENE-II PROTEIN FROM BACTERIOPHAGE-F1 Author(s): STRATHERN JN; WEINSTOCK KG; HIGGINS DR; MCGILL CR Corporate Source: NCI, FREDERICK CANC RES & DEV CTR, BASIC RES PROGRAM/FREDERICK//MD/21701 Journal: GENETICS, 1991, V127, N1, P61-73 Language: ENGLISH Document Type: ARTICLE (Abstract Available) 2/3/93 (Item 6 from file: 434) 09323349 Genuine Article#: T4208 No. References: 45 Title: FLP RECOMBINASE OF THE 2-MU-M CIRCLE PLASMID OF SACCHAROMYCES-CEREVISIAE BENDS ITS DNA TARGET - ISOLATION OF FLP MUTANTS DEFECTIVE IN DNA BENDING Author(s): SCHWARTZ CJE; SADOWSKI PD Corporate Source: UNIV TORONTO, DEPT MED GENET/TORONTO M5S 1A8/ONTARIO/CANADA/ Journal: JOURNAL OF MOLECULAR BIOLOGY, 1989, V205, N4, P647-658 Language: ENGLISH Document Type: ARTICLE 2/3/94 (Item 7 from file: 434) Genuine Article#: F8861 07863892 No. References: 37 Title: ISOLATION OF INTERMEDIATES IN THE BINDING OF THE FLP RECOMBINASE OF THE YEAST PLASMID 2-MIRON CIRCLE TO ITS TARGET SEQUENCE Author(s): ANDREWS BJ; BEATTY LG; SADOWSKI PD Corporate Source: UNIV TORONTO, DEPT MED GENET/TORONTO M5S 1A8/ONTARIO/CANADA/ Journal: JOURNAL OF MOLECULAR BIOLOGY, 1987, V193, N2, F345-358 Language: ENGLISH Document Type: ARTICLE (Item 8 from file: 434) 2/3/95 07372665

2/3/95 (Item 8 from file: 434)
07372665 Genuine Article#: C9356 No. References: 23
Title: INTERACTION OF THE FLP RECOMBINASE OF THE SACCHAROMYCES-CEREVISIAE 2-MU-M PLASMID WITH MUTATED TARGET SEQUENCES
Author(s): ANDREWS BJ; MCLEOD M; BROACH J; SADOWSKI PD
Corporate Source: UNIV TORONTO, DEPT MED GENET/TORONTO M5S
 1A8/ONTARIO/CANADA/; COLD SPRING HARBOR LAB/COLD SPRING HARBOR//NY/11724; PRINCETON UNIV, DEPT MOLEC BIOL/PRINCETON//NJ/08544
Journal: MOLECULAR AND CELLULAR BIOLOGY, 1986, V6, N7, P2482-2489

Language: ENGLISH Document Type: ARTICLE

2/3/96 (Item 9 from file: 434)

07260459 Genuine Article#: C1205 No. References: 44

Title: FLP SITE-SPECIFIC RECOMBINASE OF YEAST 2-MU-M PLASMID - TOPOLOGICAL FEATURES OF THE REACTION

Author(s): BEATTY LG; BABINEAUCLARY D; HOGREFE C; SADOWSKI PD

Corporate Source: UNIV TORONTO, DEPT MED GENET/TORONTO M5S

1A8/ONTARIO/CANADA/

Journal: JOURNAL OF MOLECULAR BIOLOGY, 1986, V188, N4, P529-544

Language: ENGLISH Document Type: ARTICLE

2/3/97 (Item 10 from file: 434)

06806789 Genuine Article#: AUF29 No. References: 22

Title: THE FLP RECOMBINASE OF THE YEAST 2-MU-M PLASMID - CHARACTERIZATION OF ITS RECOMBINATION SITE

Author(s): SENECOFF JF; BRUCKNER RC; COX MM

Corporate Source: UNIV WISCONSIN, COLL AGR & LIFE SCI, DEPT BIOCHEM, 420 HENRY MALL/MADISON//WI/53706

Journal: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, 1985, V82, N21, P7270-7274

Language: ENGLISH Document Type: ARTICLE

2/3/98 (Item 11 from file: 434)

06780315 Genuine Article#: ATE60 No. References: 28

Title: THE FLP RECOMBINASE OF THE SACCHAROMYCES-CEREVISIAE 2-MU-M PLASMID ATTACHES COVALENTLY TO DNA VIA A PHOSPHOTYROSYL LINKAGE

Author(s): GRONOSTAJSKI RM; SADOWSKI PD

Corporate Source: UNIV TORONTO, DEPT MED GENET/TORONTO M5S

1A8/ONTARIO/CANADA/

Journal: MOLECULAR AND CELLULAR BIOLOGY, 1985, V5, N11, P3274-3279

Language: ENGLISH Document Type: ARTICLE

2/3/99 (Item 1 from file: 76)

1171271 82001618771

Mutations in the 2-.mu.m circle site-specific recombinase that abolish recombination without affecting substrate recognition.

Prasad, P.V.; Young, L.-J.; Jayaram, M.

Dep. Mol. Biol., Res. Inst. Scripps Clin., 10666 N. Torrey Pines Rd., La Jolla, CA 92037, USA

PROC. NATL. ACAD. SCI. USA; 84(8), pp. 2189-2193 1987

Language: English Summary Language: English

2/3/100 (Item 1 from file: 73)

8210454 EMBASE No: 91239554

Erratum: Identification of the active site tyrosine of Flp recombinase. Possible relevance of its location to the mechanism of recombination (Vol. 265 (1990) 18504-18510)

Evans B.R.; Chen J.-W.; Parsons R.L.; Bauer T.K.; Teplow D.B.; Jayaram M. J. BIOL. CHEM. (USA) , 1991, 266/11 (7312) CODEN: JBCHA ISSN: 0021-9258

LANGUAGES: English

2/3/101 (Item 2 from file: 73)

7363228 EMBASE No: 89079376

FLP recombinase of the 2 microm circle plasmid of Saccharomyces cerevisiae bends its DNA target. Isolation of FLP mutants defective in DNA bending

Schwartz C.J.E.; Sadowski P.D.

Department of Medical Genetics, University of Toronto, Toronto, Ont. M5S

J. MOL. BIOL. (United Kingdom) , 1989, 205/4 (647-658) CODEN: JMOBA ISSN: 0022-2836

LANGUAGES: English

2/3/102 (Item 1 from file: 144)

09775158 FASCAL No.: 91-0572331

Domain of a yeast site-specific recombinase (Flp) that recognizes its target site

JING-WEN CHEN; EVANS B R; SANG-HWA YANG; TEPLOW D/ B; JAYARAM M Univ. Texas, dep. microbiology, Austin TX 78712, USA

Journal: Proceedings of the National Academy of Sciences of the United States of America, 1991, 88 (14) 5944-5948

Language: English

2/3/103 (Item 2 from file: 144)

09771721 PASCAL No.: 91-0568894

Protein-based assymmetry and protein-protein interactions in FLP recombinase-mediated site-specific recombination

XIAO-HONG QIAN; INMAN R B; COX M M

Univ. Wisconsin, coll. agricultural life sci., dep. biochemistry, Madison WI 53706, USA

Journal: Journal of biological chemistry (The), 1990, 265 (35) 21779-21788

Language: English

2/3/104 (Item 3 from file: 144)

09730857 PASCAL No.: 91-0527991

Site-specific recombination between homologous chromosomes in Drosophila GOLIC K G

Univ. Chicago, Howard Hughes medical inst., dep; molcular genetics cell biology, Chicago IL 60637, USA

Journal: Science: (Washington, DC), 1991, 252 (5008) 958-961 Language: English

2/3/105 (Item 4 from file: 144)

09563896 PASCAL No.: 91-0354326

Tyr60 variants of Flp recombinase generate conformationally altered protein-DNA complexes : differential activity in full-site and half-site recombinations

JING-WEN CHEN; EVANS B R; LEI ZHENG; JAYARAM M Univ. Texas at Austin, dep. microbiology, Austin TX 78712, USA Journal: Journal of molecular biology, 1991, 218 (1) 107-118 Language: English

2/3/106 (Item 5 from file: 144)

Interaction of the FLP recombinase of the saccharomyces cerevisiae 2 mu m

plasmid with mutated target sequences

NDREWS B J; MCLEOD M; BROACH J; SADOWSKI P D

Univ. Toronto, dep. medical genetics, Toronto ON M5S 1A8, Canada

Journal: Molecular and cellular biology, 1986, 6 (7) 2482-2489

Language: ENGLISH

2/3/107 (Item 1 from file: 77)

89015048 V17N02

FLP recombinase induction of the breakage-fusion-bridge cycle (BFBC) and gene conversion in Saccharomyces cerevisiae

Rank, G.H.; Xiao, W.; Kolenovsky, A.; Arndt, G.

Univ. Saskatchewan, Saskatoon, Sask., Canada

XVIth International Congress of Genetics 8830579 Toronto (Canada) 20-27 Aug 1988

Genetics Society of Canada; National Research Council Canada; Royal Society of Canada; Biological Council of Canada

The Proceedings of the Congress will be Published in a Special Volume of Journal Genome Poster Paper

2/3/108 (Item 2 from file: 77)

89014585 V17N02

Structure-function relationship of the sequence specific DNA binding function of the FLP recombinase

Amin, A.A.; Sadowski, P.D.

Univ. Toronto, Toronto, Ont., Canada

XVIth International Congress of Genetics 8830579 Toronto (Canada) 20-27 Aug 1988

Genetics Society of Canada; National Research Council Canada; Royal Society of Canada; Biological Council of Canada

The Proceedings of the Congress will be Published in a Special Volume of Journal Genome Poster Paper

2/3/109 (Item 3 from file: 77)

89014584 V17N02

FLP recombinase of 2 mu circle of S. cerevisiae bends its DNA target: An in vitro analysis

Schwartz, C.J.E.; Sadowski, P.D.

Univ. Toronto, Toronto, Ont., Canada

XVIth International Congress of Genetics 8830579 Toronto (Canada) 20-27 Aug 1988

Genetics Society of Canada; National Research Council Canada; Royal Society of Canada; Biological Council of Canada

The Proceedings of the Congress will be Published in a Special Volume of Journal Genome Poster Paper

2/3/110 (Item 4 from file: 77)

89013277 V17N02

Mutational analysis of the FLP site-specific recombinase of the yeast 2 micron plasmid

Sadowski, P.

Univ. Toronto, Toronto, Ont., Canada

XVIth International Congress of Genetics 8830579 Toronto (Canada) 20-27 Aug 1988

Genetics Society of Canada; National Research Council Canada; Royal

Society of Canada; Biological Council of Canada

The Proceedings of the Congress will be Published in a Special Volume of Journal Genome

2/3/111 (Item 5 from file: 77)

89012894 V17N02

Step-arrest mutants of FLP recombinase: Implications for the mechanism of recombination

Evans, B.R.; Parsons, R.; Crain, K.; Jayaram, M.

Mol. Biol. Dep., Res. Inst. Scripps Clin. and Res. Found., La Jolla, CA, USA

14th International Conference on Yeast Genetics and Molecular Biology 8830578 Espoo (Finland) 7-13 Aug 1988

European Association for Cancer Research

Subscription Department C, John Wiley & Sons Inc., 605 Third Avenue, New York, NY 10158 (USA), Abstracts will be Published in Special Issue of Journal 'Yeast' Volume 4. ISSN 0749-503X

2/3/112 (Item 1 from file: 265)

0129563 DIALOG FILE NO. 265/266 FEDERAL RESEARCH IN PROGRESS

IDENTIFYING NO.: 5R01HG00250-04 AGENCY CODE: CRISP

Directed rearrangement of the mammalian genome in vivo

PRINCIPAL INVESTIGATOR: YOUDERIAN, PHILIP A

ADDRESS: CALIF INST OF BIOLOG RESEARCH 11099 NORTH TORREY PINES ROAD LA JOLLA, CA 92037

PERFORMING ORG.: CALIFORNIA INSTITUTE OF BIOLOGICAL RES, SAN DIEGO, CALIFORNIA

SPONSORING ORG.: NATIONAL CENTER FOR HUMAN GENOME RESEARCH FY: 92 FUNDS: \$182,972

2/3/113 (Ntem 2 from file: 265)

0127425 DIALOG FILE NO. 265/266 FEDERAL RESEARCH IN PROGRESS IDENTIFYING NO.: 50016M35654-07 AGENCY CODE: CRISP Site specific recombination in the yeast plasmid 2 micron circle PRINCIPAL INVESTIGATOR: IAYARAM, MAKKUNI ADDRESS: UNIVERSITY OF TEXAS DEPT OF MICROBIOLOGY AUSTIN, TX 78712 PERFORMING ORG.: UNIVERSITY OF TEXAS AUSTIN, AUSTIN, TEXAS SPONSORING ORG.: NATIONAL INSTITUTE OF GENERAL MEDICAL SCIENCES FY: 92 FUNDS: \$265,024

2/3/114 (Item 3 from file: 265)

0020434 DIALOG FILE NO. 265/266 FEDERAL RESEARCH IN PROGRESS

IDENTIFYING NO.: 9105934; 9105934 AGENCY CODE: NSF

Genetic Analysis of Pattern Formation During Drosophila Neurogenesis

PRINCIPAL INVESTIGATOR: Ellis, Hilary M Dr.

PERFORMING ORG.: Emory University, Biology, Atlanta, GA 30322

PROJECT MONITOR: Program Manager

SPONSORING ORG.: National Science Foundation, DIV OF INTEGRATIVE BIOLOGY

& NEUROSCIENC, Washington, D.C., 20550

DATES: 910715 TO 920630 FY: 91 \ FUNDS: \$69,613

2/3/115 (Item 4 from file: 265)

0019890 PIALOG FILE NO. 265/266 FEDERAL RESEARCH IN PROGRESS

IDENTIFYING NO.: 9103946; 9103946 AGENCY CODE: NSF

Generation of Mosaicism in Mice by a Site-Specific Recombinase (FLP) PRINCIPAL INVESTIGATOR: 8 Gorman, Stephen Dr. PERFORMING ORG.: Salk Institute for Biological Studies, Gene Expression Laboratory, San Diego, CA 92128 PROJECT MONITOR: Thomas E. Brady SPONSORING ORG.: National Science Foundation, DIV OF INTEGRATIVE BIOLOGY & NEUROSCIENC, Washington, D.C., 20550 DATES: 910315 TO 920831 FY: 91 FUNDS: \$49,522 2/3/116 (Item 5 from file: 265) 0016781 DIALOG\FILE NO. 265/266 FEDERAL RESEARCH IN PROGRESS IDENTIFYING NO : 9019220; 9019220 AGENCY CODE: NSF Genetic Analysis in Arabidopsis PRINCIPAL INVESTIGATOR: Signer, Ethan R Dr. ORG.: \ Massachusetts Institute of Technology, Biology, PERFORMING Cambridge, MA 02139 PROJECT MONITOR: DeLill Nasser SPONSORING ORG.: National Science Foundation, DIV OF MOLECULAR & CELLULAR BIOSCIENCES, Washington, D.C., 20550 DATES: 910201 TO 930731 FY 91 FUNDS: \$200,000 (Item 1 from file: 35) 2/3/117 01212062 ORDER NO: AADNN-59965 THE ROLE OF DNA BENDING IN FLP-MEDIATED SITE-SPECIFIC RECOMBINATION Author: SCHWARTZ, CAROL JUDITH ELAINE Degree: PH.D. Year: 1990 Corporate Source/Institution: UNIVERSITY OF TORONTO (CANADA) (0779) Source: VOLUME 52/11-B OF DISSERTATION ABSTRACTS INTERNATIONAL. PAGE 5647. 209 PAGES 0-315-59965-0 ISBN: (Item 2 from file: 35) 2/3/118 01142876 ORDER NO: AAD90-30816 UNUSUAL DNA STRUCTURE IN SITE-SPECIFIC AND HOMOLOGOUS RECOMBINATION (RECOMBINATION) Author: UMLAUF, SCOTT W. Degree: PH.D. 1990 Year: Corporate Source/Institution: THE UNIVERSITY OF WISCONSIN - MADISON (0262) Source: VOLUME 51/09-B OF DISSERTATION ABSTRACTS INTERNATIONAL. PAGE 4199. 219 PAGES (Item 3 from file: 35) 2/3/119 1061565 ORDER NO: AAD89-12817 ANALYSIS OF THE MAJOR DNASE I HYPERSENSITIVE SITE ON THE YEAST TWO-MICRON DNA PLASMID Author: STRAND, ANDREW DAVID Degree: PH.D. Year: 1989 Corporate Source/Institution: UNIVERSITY OF MINNESOTA (0130) Source: VOLUME 50/02-B OF DISSERTATION ABSTRACTS INTERNATIONAL.

PAGE 446. 111 PAGES

2/3/120 (Item 4 from file: 35)

949308 ORDER NO: AAD87-06690

A GENETIC ANALYSIS OF FACTORS INVOLVED IN THE MAINTENANCE OF THE 2 MICRON PLASMID OF SACCHAROMYCES CEREVISIAE (CHROMATIN)

Author: VEIT, BRUCE EDWARD

Degree: PH.D. Year: 1986

Corporate Source/Institution: UNIVERSITY OF WASHINGTON (0250) Source: VOLUME 47/12-B OF DISSERTATION ABSTRACTS INTERNATIONAL.

PAGE 4763. 97 PAGES

2/3/121 (Item 1 from file: 51) 00405585 91-03-b0028 SUBFILE: FSTA

Yeast 2 MUm vectors replicate and undergo recombination in Torulaspora delbrueckii.

Compagno, C.; Ranzi, B. M.; Martegani, E.

Correspondence (Reprint) address, B. M. Ranzi, Dipartimento di Fisiologia e Biochimica Generali, Sezione di Biochimica Comparata, Univ. di Milano, Milan, Italy

Molecular Microbiology 1989 , 3 (8) 1003-1010 LANGUAGE: English

2/3/122 (Item 1 from file: 60)

09154644

PROJ NO: NYC-186301 AGENCY : SAES NY.C

PROJ TYPE: STATE

START: 01 JUL 91 TERM: 30 JUN 92

INVEST: MACINTYRE R J

ENTOMOLOGY

CORNELL UNIVERSITY

ITHACA NEW YORK 14853

DEVELOPMENT OF A MORE EFFICIENT INSECT TRANSFORMATION SYSTEM

OBJECTIVES: The goal of the research described below is to develop a system in which DNA canbe both easily and effectively delivered to insect embryos and, using the yeast "flip recombinase" system, insure the recovery of transgenic animals at high frequencies.

PRIMARY HEADINGS: R207 Insect Control-Field Crops; A4500 Protection Against Insects; C6500 Invertebrates; F1313 Physiology-Other

2/3/123 (Item 2 from file: 60)

09091400

PROJ NO: WIS02827 AGENCY : SAES WIS

PROJ TYPE: STATE

START: 01 JUL 86 TERM: 30 NOV 96

FY: 1989

INVEST: COX M M

BIOCHEMISTRY

UNIV OF WISCONSIN

MADISON WISCONSIN 53706

THE BIOCHEMISTRY OF GENETIC RECOMBINATION

OBJECTIVES: The FLP recombinase (derived from yeast) has been purified extensively. The properties of this protein and the recombination event it catalyzes are being studied in vitro. The recombination site utilized by this protein has been defined in detail. Studies on the mechanism of action of this recombination system are now getting underway.

PRIMARY HEADINGS: R318 Noncommodity Biotechnology, Biometry; A7000 Experimental Design, Statistical Methods; C6300 Biological Cell Systems; F0114 Biochemistry and Biophysics-Other

2/3/124 (Item 1 from file: 286)
0050984 Journal Announcement: 08APR91 Doc Type: 2
Nature, 15 MAR 1991, Vol(No) 251(4999), Page(s) 1351-1355

1ST COMPANY/ORGANIZATION NAME:
Salk Institute for Biological Studies, The, USA (1921)?

YSCPLASM 6318 bp DNA circular PLN 31-JUL-1992 DEFINITION Yeast (S.cerevisiae) 2 micron circle plasmid, complete genome. ACCESSION J01347 L00321 L00322 L00323 L00324 M10185 M11111 M11593 M14239 M14240 M14241 M14242 M14243 M14244 M14245 M14253 M14254 M14255 M14256 M14257 M14258 M14259 M14591 M14592 M14593 M14594 M14595 M14596 M14597 M14598 V01323 KEYWORDS DNA-binding protein; Rep-1 protein; Rep-2 protein; circular; complete genome; d protein; plasmid; protein FLP; recombinase; repeat region. SOURCE Yeast (S.cerevisiae, strain A364A D5) DNA, clones pJDB71, p82-6B, CV20, pMMD2, pGP20, pJFS166 (see comment). ORGANISM Saccharomyces cerevisiae Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Endomycetales; Saccharomycetaceae. REFERENCE 1 (bases 1 to 1022) AUTHORS Hindley, J. and Phear, G.A. TITLE Sequence of 1019 nucleotides encompassing one of the inverted repeats from the yeast 2 micron plasmid JOURNAL Nucleic Acids Res. 7, 361-375 (1979) MEDLINE 80034481 REFERENCE 2 (bases 1 to 6318; 1 to 6318) AUTHORS Hartley, J.L. and Donelson, J.E. TITLE Nucleotide sequence of the yeast plasmid JOURNAL Nature 286, 860-865 (1980) MEDLINE 81012161 REFERENCE 3 (bases 3891 to 3990) AUTHORS Broach, J.R., Guarascio, V.R. and Jayaram, M. TITLE Recombination within the yeast plasmid 2-micron circle is site-specific JOURNAL Cell 29, 227-234 (1982) MEDLINE 82259368 REFERENCE 4 (bases 3881 to 4020) AUTHORS McLeod, M., Volkert, F. and Broach, J.R. TITLE Components of the site-specific recombination system encoded by the yeast plasmid 2-micron circle JOURNAL Cold Spring Harb. Symp. Quant. Biol. 49, 779-787 (1984) MEDLINE 85153059 REFERENCE 5 (bases 670 to 732) AUTHORS Andrews, B.J., Proteau, G.A., Beatty, L.G. and Sadowski, P.D. TITLE The FLP recombinase of the 2 micron circle DNA of yeast: Interaction with its target sequences JOURNAL Cell 40, 795-803 (1985) MEDLINE 85176933 REFERENCE 6 (bases 5570 to 5605) AUTHORS Babineau, D., Vetter, D., Andrews, B.J., Gronostajski, R.M., Proteau, G.A., Beatty, L.G. and Sadowski, P.D. TITLE The FLP protein of the 2-micron plasmid of yeast: Purification of the protein from Escherichia coli cells expressing the cloned FLP gene JOURNAL J. Biol. Chem. 260, 12313-12319 (1985) MEDLINE 86008307 REFERENCE 7 (sites) AUTHORS Gronostajski, R.M. and Sadowski, P.D. TITLE Determination of DNA sequences essential for FLP-mediated recombination by a novel method JOURNAL, J. Biol. Chem. 260, 12320-12327 (1985) MEDLINE 86008308

Ook bNA? 80 ASS

QH301. CC

REFERENCE 8 (sites)

AUTHORS Sutton, A. and Broach, J.R.

TITLE Signals for transcription initiation and termination in the Saccharomyces cerevisiae plasmid 2 micron circle

JOURNAL Mol. Cell. Biol. 5, 2770-2780 (1985)

MEDLINE 86284639

REFERENCE 9 (sites)

AUTHORS Gronostajski, R.M. and Sadowski, P.D.

TITLE The FLP recombinase of the Saccharomyces cerevisiae 2-micron plasmid attaches covalently to DNA via a phosphotyrosyl linkage

JOURNAL Mol. Cell. Biol. 5, 3274-3279 (1985)

MEDLINE 86310798

REFERENCE 10 (bases 667 to 739)

AUTHORS Senecoff, J.F., Bruckner, R.C. and Cox, M.M.

TITLE The FLP recombinase of the yeast 2-micron-m plasmid: Characterization of its recombination site

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 82, 7270-7274 (1985)

MEDLINE 86042647

REFERENCE 11 (sites)

AUTHORS McLeod, M., Craft, S. and Broach, J.R.

TITLE Identification of the crossover site during FLP-mediated recombination in the Saccharomyces cerevisiae plasmid 2 micron circle

JOURNAL Mol. Cell. Biol. 6, 3357-3367 (1986)

MEDLINE 87089667

COMMENT [8] sites; mRNA CAP sites and poly-adenylation sites. [9] sites; FLP binding.

[7] sites; FLP cleavage.

[11] sites; FLP-mediated recombination crossover site. Draft entry and clean copy sequence for [5] kindly provided by J.Senecoff, 24-JAN-1986.

Yeast 2 micron plasmid contains two 599 bp inverted repeats separated by a large unique (UL) and a small unique (US) region. During recombination the UL and US regions invert producing two sequence forms that differ in the orientation of one unique region relative to the other. The A form is presented below. FLP is the only 2-micron circle-encoded protein needed for specific site recombination between the IRs of 2-micron circle. The minimal size of the recombination site required for efficient FLP recombinase-catalyzed recombination in vitro is no more than 28 bp, which includes parts of two 13 bp inverted repeats (positions 690-702 and 711-723) and all of an 8 bp spacer (703-710) [5]. The FLP recombinase cleaves the DNA at the boundaries of the spacer and becomes covalently linked to the spacer DNA [5], [9]. The efficiency of the recombination is reduced if the spacer in a recombinant site is increased or decreased by 1 bp. while the spacer in the second site is unaltered [5]. Recombination between two sites with identical 1-base pair additions or deletions is relatively unaffected, suggesting that pairing of sequences in the spacer regions is important in FLP-promoted recombination events [5]. The sequence asymmetry utilized by the recombinase to determine the orientation of the site is located uniquely within the spacer region. Another 13 bp direct repeat, is found at positions 676-688 [5]. FLP-mediated recombination involving two FLP sites that are inverted with respect to each other results in inversion of the DNA sequences between the sites [4]. If the participating recombination sites are in direct orientation, FLP

A start codon in phase with the Rep1 coding region is located at positions 1966-1964. Two CAP sites for Rep1 mRNA are located beyond the 'atg' codon (position 2008) at positions 2004 and 2005. Complete source information: Yeast (S.cerevisiae, strain A364A D5) DNA, clones pJDB71 [1], p82-6B [2], CV20 [3], pMMD2 [4], pGP20 [5], pJFS166 [10]. NCBI gi: 172190 **FEATURES** Location/Qualifiers 1..6318 source /organism="Saccharomyces cerevisiae" 1..545 exon conflict replace((157.160)..(157.160),**) /citation=[1] replace((289.290)..(289.290),**) conflict /citation=[1] repeat_region 341..939 /note="IR2" replace((464.466)..(464.466),"") conflict /citation=[1] replace(558,"") conflict /citation=[1] conflict replace(561,"") /citation=[1] conflict replace((622.624)..(622.624),**) /citation=[1] replace(642,"") conflict /citation=[1] conflict replace((665.666)..(665.666),**) /citation=[1] misc binding 673..722 /note="FLP recombinase binding site A [9]" /bound_moiety="FLP recombinase" conflict replace((793.794)..(793.794),") /citation=[1] complement(836..2038) mRNA /note="Rep1 mRNA (alt.)" mRNA complement(836..2017) /note="Rep1 mRNA (alt.)" mRNA complement(836..2019) /note="Rep1 mRNA (alt.)" complement(836..2010) mRNA /note="Rep1 mRNA (alt.)" mRNA complement(836..2004) /note="Rep1 mRNA (alt.)" mRNA complement(836..2005) /note="Rep1 mRNA (alt.)" CDS complement(887..2008) /note="Rep 1 protein; NCBI gi: 172192" /codon_start=1 /db_xref="PID:g172192" /translation="MNGERLLACIKQCIMQHFQPMVYDESRCVIETTRGTFPVPDNYK KYKTLAFAFVGHVLNTDDTPVIEKELDWPDPALVYNTIVDRIINHPELSQFISVAFIS QLKATIGEGLDINVKGTLNRRGKGIRRPKGVFFRYMESPFVNTKVTAFFSYLRDYNKI

promotes only the excision of the intervening DNA sequences [4]. The Rep 1 and Rep proteins are involved plasmid partitioning and

protein stability.

```
ELPPEEDPSRELNNVQHEVNSLTEQDAEADEGLWGEIDSLCEKWQSEAEDQTEAEIIA
        DRIIGNSQRMANLKIRRTKFKSVLYHILKELIQSQGTVKVYRGSSFSHDSIKISLHYE
        EQHITAVWYLTVKFEEHWKPVDVEVEFRCKFKERKVDG"
mRNA
           2254..2841
        /note="D mRNA (alt.; 5' end +/- 3 bp)"
mRNA
           2254..2861
        /note="D mRNA (alt.; 5' end +/- 3 bp)"
CDS
          2271..2816
        /note="D protein; NCBI gi: 172193"
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        /db_xref="PID:g172193"
        /translation="MPYKTAIDCIEELATQCFLSKLTDDDVSTFRRVCSKENDIIKLA
        LRIPRTIDYTSILRLLYDTLPLRSLSFNEALPLFCYSIDPAQQRQCDLRFYLRDVVKL
        ARPRKRLEMQKALLQWLPSLLSDVTLQLLNDIRIRFEEIQPNIRQTVLQIYDRTCYPS
        LNFEHPNLGVFPETDSIFEPV*
repeat_region 3714..4312
        /note="IR1"
misc_binding 3930..3979
        /note="FLP-recombinase binding site B [9]"
        /bound_moiety="FLP recombinase"
mRNA
           complement(4108..5182)
        /note="REP2 mRNA (major alt.)"
           complement(4108..5183)
mRNA
        /note="REP2 mRNA (major alt.)"
           complement(4108..5184)
mRNA
        /note="REP2 mRNA (major alt.)"
           complement(4108..5223)
mRNA
       /note="REP2 mRNA (minor alt.)"
           complement(4108..5195)
mRNA
        /note="REP2 mRNA (major alt.)"
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mRNA
        /note="REP2 mRNA (major alt.)"
mRNA
           complement(4108..5196)
        /note="REP2 mRNA (major alt.)"
           complement(4108..5197)
mRNA
        /note="REP2 mRNA (major alt.)"
           complement(4108..5212)
mRNA
        /note="REP2 mRNA (minor alt.)"
CDS
          complement(4308..5198)
        /note="Rep 2 protein; NCBI gi: 172194"
        /codon_start=1
        /db_xref="PID:g172194"
        /translation="MDDiETAKNLTVKARTAYSVWDVCRLFIEMIAPDVDIDIESKRK
        SDELLFPGYVIRPMESLTTGRPYGLDSSAEDSSVSSDSSAEVILPAAKMVKERFDSIG
        NGMLSSQEASQAAIDLMLQNNKLLDNRKQLYKSIAIIIGRLPEKDKKRATEMLMRKMD
        CTQLLVPPAPTEEDVMKLVSVVTQLLTLVPPDRQAALIGDLFIPESLKDIFNSFNELA
        AENRLQQKKSELEGRTEVNHANTNEEVPSRRTRSRDTNARGAYKLQNTITEGPKAVPT
        KKRRVATRVRGRKSRNTSRV*
mRNA
           join(5549..6318,1..545)
        /note="Flp mRNA"
          5549..6318
exon
          join(5570..6318,1..523)
CDS
        /note="recombinase (FLP); NCBI gi: 172191"
        /codon_start=1
       /db_xref="PID:g172191"
```

/translation="MPQFGILCKTPPKVLVRQFVERFERPSGEKIALCAAELTYLCWM"

ASEYHNNTKFILTFSCQAYWASGPNFSALKNVIRCSIIHEYISKFVEREQDKGHIGDQ

ITHNGTAIKRATFMSYNTIISNSLSFDIVNKSLQFKYKTQKATILEASLKKLIPAWEF TIIPYYGQKHQSDITDIVSSLQLQFESSEEADKGNSHSKKMLKALLSEGESIWEITEK ILNSFEYTSRFTKTKTLYQFLFLATFINCGRFSDIKNVDPKSFKLVQNKYLGVIIQCL VTETKTSVSRHIYFFSARGRIDPLVYLDEFLRNSEPVLKRVNRTGNSSSNKQEYQLLK DNLVRSYNKALKKNAPYSIFAIKNGPKSHIGRHLMTSFLSMKGLTELTNVVGNWSDKR ASAVARTTYTHQITAIPDHYFALVSRYYAYDPISKEMIALKDETNPIEEWQHIEQLKG SAEGSIRYPAWNGIISQEVLDYLSSYINRRI*

old_sequence replace(5583,"")

/citation=[2]

BASE COUNT 1876 a 1284 c 1179 g 1979 t

ORIGIN 1 bp upstream of EcoRI site.

1 gaattotgaa coagtootaa aacgagtaaa taggacoggo aattottoaa goaataaaca

- 61 ggaataccaa ttattaaaag ataacttagt cagatcgtac aataaagctt tgaagaaaaa
- 121 tgcgccttat tcaatctttg ctataaaaaa tggcccaaaa tctcacattg gaagacattt
- 181 gatgacctca tttctttcaa tgaagggcct aacggagttg actaatgttg tgggaaattg
- 241 gagcgataag egtgettetg eegtggeeag gacaacgtat acteateaga taacagcaat
- 301 acctgateae taettegeae tagttteteg gtaetatgea tatgateeaa tateaaagga
- 361 aatgatagca ttgaaggatg agactaatcc aattgaggag tggcagcata tagaacagct
- 421 aaagggtagt gctgaaggaa gcatacgata ccccgcatgg aatgggataa tatcacagga
- 481 ggtactagac tacctttcat cctacataaa tagacgcata taagtacgca tttaagcata
- 541 aacacgcact atgccgttct tctcatgtat atatatatac aggcaacacg cagatatagg
- 601 tgcgacgtga acagtgagct gtatgtgcgc agctcgcgtt gcattttcgg aagcgctcgt
- 661 tttcggaaac gctttgaagt tcctattccg aagttcctat tctctagaaa gtataggaac
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- 961 caaatttac tgtcaagtag acccatacgg ctgtaatatg ctgctcttca taatgtaagc
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- 1861 ctaacgtttt gtattictta taattgtcag gaactggaaa agtccccctt gtcgtctcga
- 1921 ttacacacct actticateg tacaccatag gitggaagtg etgeataata cattgettaa
- 1981 tacaagcaag cagtototog coattoatat ttoagttatt ttocattaca gotgatgtoa
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